

FISHERIES INVESTIGATIONS IN LAKES AND STREAMS



ANNUAL PROGRESS REPORT

Statewide Freshwater Fishery Research

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Study Title: STATEWIDE FISHERIES RESEARCH
Job Title: Hydroacoustic Evaluation of Santee-Cooper Lakes
Period Covered October 1, 2013 - September, 30 2014

Summary

Sixteen hydroacoustic transects of lakes Marion and Moultrie were completed in 2013. Of these, 8 transects provided good estimates of standing crop of pelagic fishes. The average standing crop observed in 2013 was 51 kg/ha, which was substantially less than observed in preliminary evaluations conducted in 2010. Gill nets were used to sample species composition and indicated that threadfin shad *Dorosoma petenense* accounted for approximately 80% of the standing crop and the production.

Introduction

To understand fish population dynamics in the Santee-Cooper system, knowledge of the standing crop (kg/ha) and production is essential. Hydroacoustic technology allows these estimates to be made on the vast expanses of the Santee-Cooper lakes. Preliminary sampling in 2010 verified that the use of this technology on Santee-Cooper was practical. This report summarizes results obtained in the study year.

Materials and Methods

Hydroacoustic and concurrent gill net sampling of lakes Marion and Moultrie were conducted in summer and fall of 2013 with a Biosonics DTX system. Hydroacoustic transects, 6 to 8 km in length, were defined, three on Lake Marion and two on Lake Moultrie. Transect locations were defined as:

1. Eutaw Creek (EC), L. Marion, 33.44114, -80.36458 to 33.44168, -80.28794
2. Stump-Free Channel (SF), L. Marion, 33.48837, -80.27969 to 33.51086, -80.19805
3. Along dike and dam (DK), L. Marion, 33.51549, -80.18845 to 33.44925, -80.16536
4. West Dike (WD), L. Moultrie, 33.35431, -80.04438 to 33.29497, -80.08909
5. Bonneau to Pinopolis (PI), L. Moultrie, 33.30005, -79.99644 to 33.24618, -80.01282.

Hydroacoustic transects were initiated 45 minutes after sunset. In August of 2013, individual down-looking and the side-looking transects were conducted. Beginning in September 2013, the down-looking and side-looking transects were conducted simultaneously, as appropriate cabling was secured and put in place. Digital files from the completed transects were sent to an outside contractor, Aquacoustics Inc., for processing and analysis.

Gill net sampling was conducted concurrently with hydroacoustic transects. Initially (August 2013), a 6 foot deep experimental gill net with 15 foot sections of 0.375, 0.500, 0.625, and 0.750 inch bar mesh was used. Cast nets with 0.25 and 0.375 inch mesh were also used in August 2013 to sample fish. Beginning in September, 2013, a 15 foot panel of 0.25 inch bar mesh netting was added to the experimental gill net; this configuration was used for the remainder of the sampling season. Generally, two floating, experimental gill nets were set at distinct locations along the hydroacoustic transect. However, on several occasions, a near-bottom gill net was set to compare surface vs. near-bottom catches. Once the nets were retrieved, the catch was removed from the net, placed on ice, and brought to the laboratory for measurement of length and weight. For clupeid fishes (threadfin shad, American shad *Alosa sapidissima*, blueback herring *Alosa aestivalis*, Atlantic menhaden *Brevoortia tyrannus*, and gizzard shad *Dorosoma cepedianum*), a random sample of 30 from each mesh was measured (total length (TL), mm) and weighed (to 0.1 grams (g)). Then, a random sample

of the 20 was measured. If additional fish from a species remained within a mesh, they were enumerated.

For American shad, blueback herring, threadfin shad, Atlantic menhaden and all four species combined, we determined the relationship between length and weight by log₁₀ transforming the data and using linear regression to find the line of best fit for the equation:

$$\text{Log}_{10} \text{ Weight (g)} = a + (b * \log_{10} \text{ total length (mm)})$$

The derived equation that incorporated all clupeids was used to convert observed length of hydroacoustic targets (from hydroacoustic surveys) to weight. Also, we used this equation to calculate relative condition factor, defined as observed weight divided by predicted weight, of American shad, blueback herring, and threadfin shad by sampling date and location.

Growth of threadfin shad and age-0 American shad and blueback herring was estimated by calculating the mean length of each species by each unique sampling event. Cast net data obtained in August was included. Length frequency assessment was used to distinguish age-1 from age-0 threadfin shad.

Production (P) of each threadfin shad cohort was estimated using the equation:

$$P = G * \Delta t * B$$

where,

P = production of new tissue

G = instantaneous growth rate (i.e. = $\log_e \text{ weight}_{\text{end}} - \log_e \text{ weight}_{\text{begin}}$)

Δt = the time period

B = average biomass (as obtained through hydroacoustic survey)

Results and Discussion

Start-up issues and weather caused some difficulties with hydroacoustic sampling in 2013. Sampling was scheduled to start in July but had to be moved back to August, due to electrical issues with the boat. Transducer cabling issues were not resolved until September, thus, in August, the side-look and down-look transducers could not be operated concurrently. Weather, especially thunderstorms and wind, were troublesome, as windy conditions were not suitable for obtaining good results from the side-looking transducer. However, the overall goal of conducting 16 hydroacoustic transects was met in 2013 (Table 1).

Using the eight sampling dates where good data was obtained from both down- and side-looking transducers and water temperatures were above 15 C, we obtained mean abundance and biomass estimates of 15,580 fish/ha (95% confidence interval = 9,808 to 21,352) and 51 kg/ha (95% confidence interval = 20 to 82 kg/ha) (Table 2). Biomass and numerical abundance estimates were obtained on 10 of 16 sampling dates (Table 2). Of these 10 sampling dates, exceptionally low estimates were obtained on Nov 25 and Dec 11 when water temperatures were below 15 C. We perceived that these low estimates were due to tight schooling of threadfin shad as water temperatures decline, thus, those two samples were deleted.

These abundance estimates are substantially lower than obtained during a preliminary study of Santee-Cooper in October, 2010, when mean biomass was 123 kg/ha (N = 4 transects). A question that needs further evaluation is whether the magnitude of this difference is accurate, is due to sampling variability, or is due to sample processing inconsistencies. For now, it is reasonable to assume a real difference between the two study years.

Table 1. Hydroacoustic sampling results for the Santee Cooper lakes in 2013. Site locations are defined in text.

Date, 2013	Lake	Site	Hydroacoustic (D=downlook, S=sidelook)	Gill nets (S=sinking, F= floating)	Cast Net	Water temp. (C)
Aug 7	Marion	EC	D, S	3 F	Yes	27.6
Aug 14	Marion	SF	D	0	No	28.7
Aug 21	Moultrie	PI	D, S	2 F	Yes	28.4
Aug 22	Marion	SF	S	0	Yes	-
Aug 27	Moultrie	WD	D	1 F	No	-
Aug 28	Marion	DK	D, S	2 F	Yes	-
Sept 18	Marion	DK	D,S	2 F	No	-
Sept 24	Moultrie	PI	D, S	1 S, 1 F	No	-
Oct 1	Moultrie	WD	D, S	1 S, 1 F	No	-
Oct 3	Moultrie	PI	D, S	1 S, 1 F	No	24.1
Oct 15	Marion	EC	D, S	1 S, 1 F	No	22.5
Oct 22	Marion	SF	D, S	1 F	No	22.7
Oct 22/23	Marion	DK	D,S	1 F	No	22.7
Nov 14	Moultrie	PI	D, S	1 S, 1 F	No	16
Nov 25	Marion	DK	D, S	1 S, 1 F	No	13
Dec 11	Marion	DK	D, S	2 F	No	12.3
Dec 12	Moultrie	PI	D, S	2 F	No	12.4

Table 2. Hydroacoustic results from 2013 sampling transects on lakes Marion and Moultrie, SC., using down- and side-looking transducers. Sampling sites are defined in text. 'Down' refers to estimates derived from only the down-looking transducer.

Date	Lake	Site	Biomass Kg/ha	Biomass Kg/ha (Down ¹)	Density #/ha	Mean Total Length (mm)	Mean Weight (g)
8/7	Marion	EC	12.1	6.6	5,800	45	2.4
8/14	Marion	SF	110.5	13.3	30,510	47	2.6
8/21	Moultrie	PI	43.3	27.5	18,560	44	1.9
8/27	Moultrie	WD		81.3	19,462 ^D	58	4.1
8/28	Marion	DK		40.0	11,637 ^D	49	3.1
9/18	Marion	DK	133.2	14.7	20,441	43	4.0
9/24	Moultrie	PI	32.1	10.6	16,131	44	2.4
10/1	Moultrie	WD		10.7	10,690 ^D	45	2.7
10/3	Moultrie	PI	16.2	6.5	8,270	42	2.1
10/15	Marion	EC	26.6	1.1	6,922	59	6.3
10/22	Marion	SF		2.6	2,561 ^D	62	5.9
10/23	Marion	DK		10.2	12,372 ^D	55	3.9
11/14	Moultrie	PI	35.1	13.1	18,008	60	5.3
11/25	Marion	DK	2.0	1.7	1,807	70	6.7
12/11	Marion	DK	3.5	1.0	1,463	70	8.2
12/12	Moultrie	PI		8.0	7,990 ^D	72	7.9

August sampling, with cast and gill nets, confirmed that small mesh gill netting was an effective technique and revealed that young of year blueback herring were not vulnerable to the smallest mesh in the gill net. Thus, a 0.25 inch bar mesh panel was added to the gill net for September through December gill netting; cast netting was discontinued during these months.

September through December gill net surveys indicated that threadfin shad were the dominant species in the Santee-Cooper lakes. A total of 3,296 fish were collected. Threadfin shad comprised 79.2% of the catch. Blueback herring, American shad, blue catfish *Ictalurus furcatus*, and Atlantic menhaden comprised 9.7, 8.2, 1.1, and 1.0 % of the catch, respectively. Alewife *Alosa pseudoharengus*, Gizzard shad, and channel catfish *Ictalurus punctatus* were also captured, but comprised less than 1% of the total catch. Of the specimens that were weighed, mean weight of threadfin shad, American shad, and blueback herring was 10.15 (N= 1,416), 6.06 (N= 328), and 2.11 (N= 196) grams, respectively. Based on mean weight and percent numerical abundance, 90.3, 4.2, and 1.9% of the estimated biomass was attributed to threadfin shad, American shad, and blueback herring.

In 2013, it was uncertain whether gill netting, cast netting, or another gear would be the method of choice to estimate species composition. It quickly became evident that gill netting would yield good results. However, there was experimentation during the season with the vertical positioning of the net within the water column. Based on 2013 results, future studies should set one floating and mid-water net.

The length weight relationship was calculated for all clupeids caught from August through December in both gill and cast nets. The relationships were:

Threadfin shad, $\text{Log}_{10}\text{TL (mm)} = -3.766 + (2.385 * \text{log}_{10}\text{WT (g)})$; N=1,414; $R^2=0.83$

Blueback herring, $\text{Log}_{10}\text{TL (mm)} = -4.209 + (2.522 * \text{log}_{10}\text{WT (g)})$; N=194; $R^2=0.88$

American shad, $\text{Log}_{10}\text{TL (mm)} = -4.281 + (2.606 * \log_{10}\text{WT (g)})$; N=328; $R^2=0.95$

Atlantic menhaden, $\text{Log}_{10}\text{TL (mm)} = -4.605 + (2.853 * \log_{10}\text{WT (g)})$; N=96; $R^2=0.94$

All above clupeids, $\text{Log}_{10}\text{TL (mm)} = -4.601 + (2.799 * \log_{10}\text{WT (g)})$; N=2,054; $R^2=0.89$.

The length-weight relationship for 'all clupeids' was used to convert hydroacoustic target strength to estimated weight.

Relative condition factors differed by location and time of year (Table 3, Figure 1). Both blueback herring and American shad had their lowest average condition factor at the most downlake location (PI) in Lake Moultrie (Table 3). American shad relative condition factor at the PI sampling site demonstrated a declining trend over the sampling season (Figure 1). Conversely, threadfin shad had their lowest average condition factors at the two most uplake locations (EC and SF) in Lake Marion and their highest value at the PI sampling site. The data suggests that condition of American shad declines as they migrate downstream; additional analysis is needed to fully evaluate this.

Table 3. Relative condition factor of American shad (AMS), blueback herring (BLH) and threadfin shad (TFS) in 2013 at sampling sites in Lake Marion (MA) and Lake Moultrie (MO). Number of observations in parentheses. Location of specific sampling sites defined in text.

Species	Sampling site - Lake				
	EC - MA	SF - MA	DK - MA	WD - MO	PI - MO
AMS	1.01 (91)	1.02 (39)	1.07 (74)	1.06 (19)	0.96 (104)
BLH	0.99 (27)	1.02 (14)	1.15 (47)	1.00 (17)	0.93 (92)
TFS	0.94 (323)	0.94 (141)	1.02 (322)	1.01 (194)	1.04 (434)

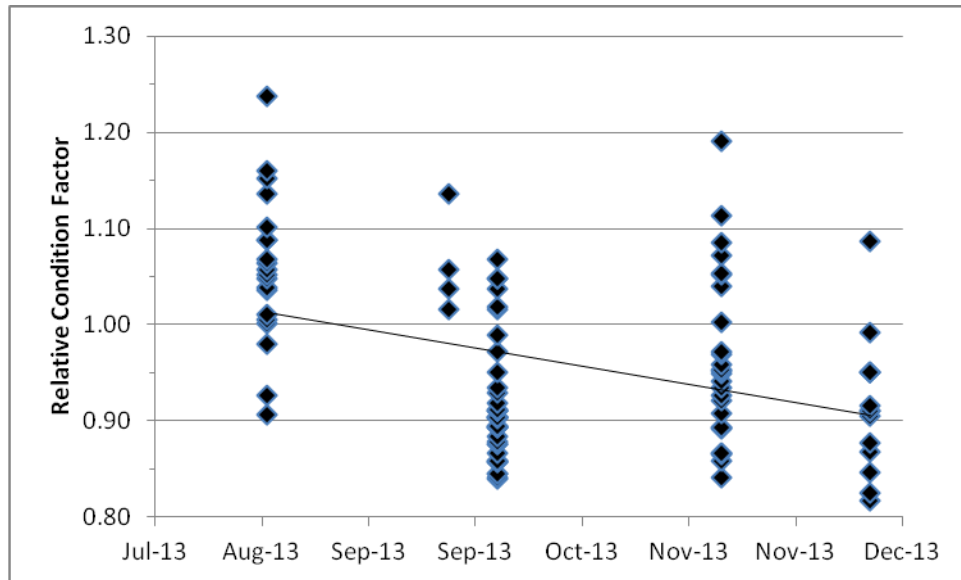


Figure 1. Relative condition factor of age-0 American shad collected in 2013 from Lake Moultrie, SC, at station PI, the location of which is defined in text.

Total length (mm) of American shad steadily increased (0.25 mm/day) during the sampling season (Figure 2), exhibiting a highly significant ($P = 0.01$) linear relationship of:

$$TL \text{ (mm)} = -10388.6 + (0.25209 * \text{day of year}),$$

where Aug 7, 2013 = 41493 and Dec 12, 2013 = 41620.

Using the above equation, predicted total length on August 7 was 71.4 mm and 103.4 mm on December 12.

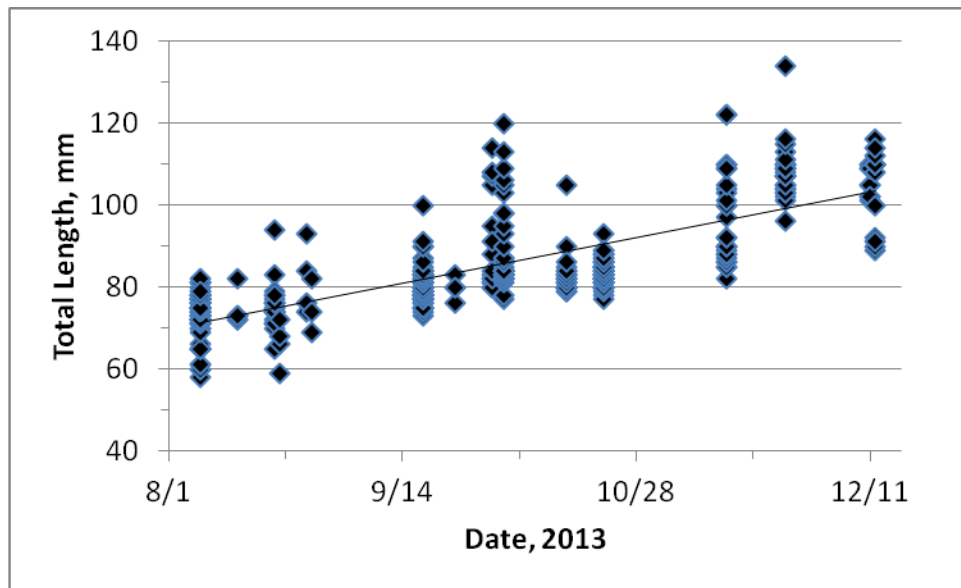


Figure 2. Growth of American shad in lakes Marion and Moultrie in 2013.

Total length (mm) of blueback herring steadily increased (0.20 mm/day) during the sampling season (Figure 3), exhibiting a highly significant ($P = 0.01$) linear relationship of:

$$TL \text{ (mm)} = -8338.26 + (0.20222 * \text{day of year}),$$

where Aug 7, 2013 = 41493 and Dec 12, 2013 = 41620.

Using the above equation, predicted total length on August 7 was 52.4 mm and 78.0 mm on December 12.

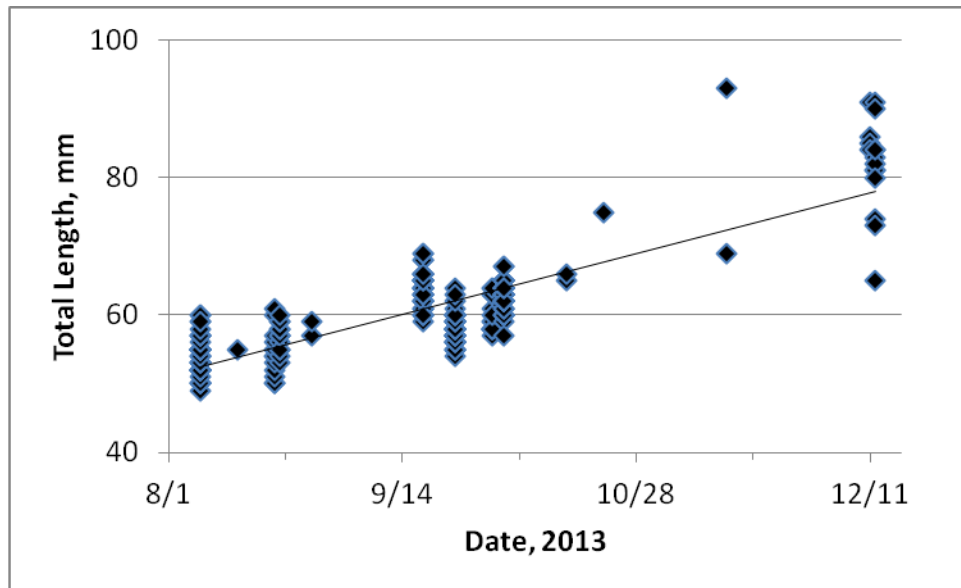


Figure 3. Growth of blueback herring in lakes Marion and Moultrie in 2013.

Length-frequency analysis indicated that threadfin shad had at least two age classes (Table 4). Based on the length-frequency analysis break points, I defined age-0 as less than 100 mm total length for August through October and less than 110 mm total length for November and December. Age 1 was defined as greater than or equal to 100 mm for August through October and greater than or equal to 110 mm for November and December, realizing that the category 'age 1' could contain age 2 or older fish. Based on this categorization, there were 1,564 age-0 and 852 age-1 threadfin shad in the measured population samples.

Table 4. Length-frequency of threadfin shad in lakes Marion and Moultrie, 2013. TL designates total length.

TL, cm.	Number				
	August	September	October	November	December
5	1		1		
6	28				
7	322	3	72		3
8	188	44	130	1	2
9	179	130	228	24	51
10	40	33	61	30	42
11	120	101	81	9	8
12	161	54	98	10	26
13	24	13	38	7	33
14	5	3	4		4
15			2		

The length distribution of threadfin shad by mesh indicated that 84.6, 98.6, 89.1, and 4.2% of the 0.25, 0.375, 0.50, and 0.625 inch mesh was age 0; the remainder were age 1. A total of 2,164 threadfin shad were not measured; based on the measured sample, 1,873 were age 0 and 291 were age 1. Adding these amounts to the measured sample indicated a total of 3,437 (75% of total) age-0 and 1,143 (25% of total) age-1 threadfin shad were sampled in 2014. Assuming equal recruitment in 2013 and 2014, these data suggest an annual total mortality of 67% for threadfin shad, or an instantaneous rate of mortality (Z) of 1.10. One would expect estimated mortality to increase during years that include a winterkill season.

Total length (mm) of age-0 threadfin shad steadily increased (0.16 mm/day) during the sampling season (Figure 4), exhibiting a highly significant ($P = 0.01$) linear relationship of:

$$TL \text{ (mm)} = -6363.5 + (0.15518 * \text{day of year}),$$

where Aug 7, 2013 = 41493 and Dec 12, 2013 = 41620.

Using the above equation, predicted total length on August 7 was 75.6 mm and 95.3 mm on December 12.

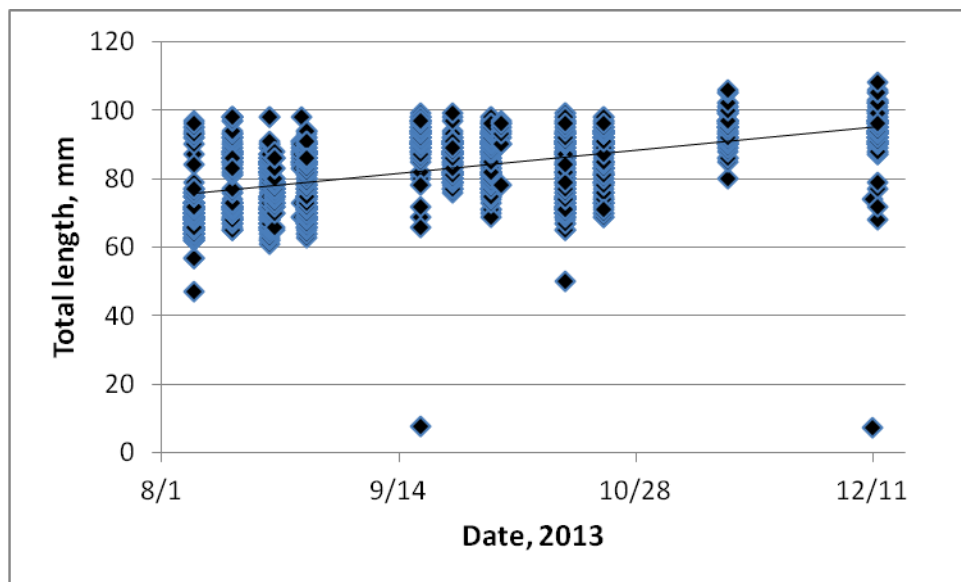


Figure 4. Growth of age-0 threadfin shad in lakes Marion and Moultrie, 2013.

Total length (mm) of age-1 threadfin shad steadily increased (0.07 mm/day) during the sampling season (Figure 5), exhibiting a highly significant ($P = 0.01$) linear relationship of:

$$TL \text{ (mm)} = -2670.7 + (0.06709 * \text{day of year}),$$

where Aug 7, 2013 = 41493 and Dec 12, 20013 = 41620.

Using the above equation, predicted total length on August 7 was 113.1 mm and 121.7 mm on December 12.

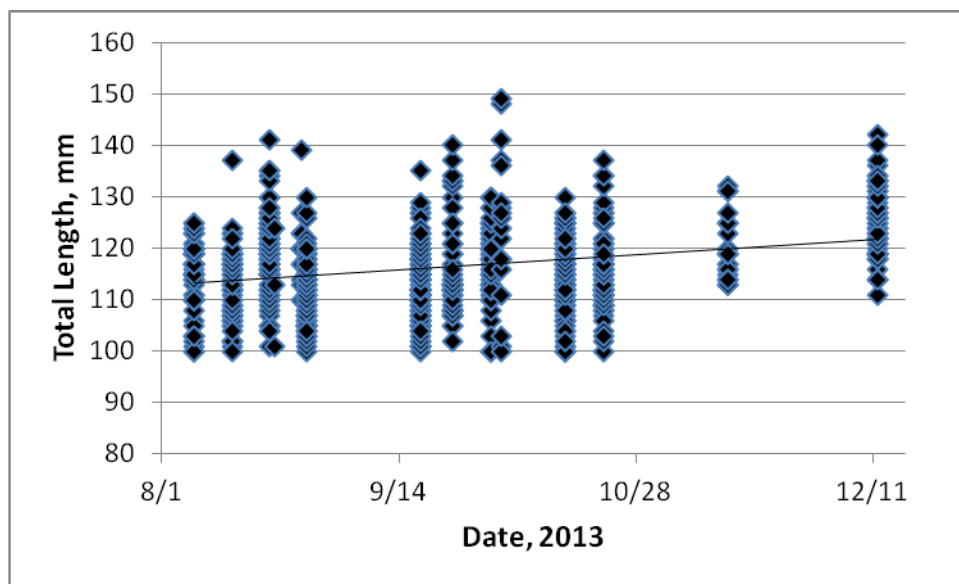


Figure 5. Growth of age-1 threadfin shad in lakes Marion and Moultrie, 2013.

Growth estimation of the two cohorts of threadfin shad is viewed as an initial estimate that has some bias due to the exclusive use of the length-frequency distribution to determine age. In future years, this analysis would benefit from aging of samples to help confirm estimated age.

Production of threadfin shad, American shad, and blueback herring during the August 7 through December 12 sampling period was estimated at 24.1 kg/ha, which is approximately 50% of the average estimated biomass of these species of 49.2 kg/ha. Age-0 threadfin shad accounted for 79% of this production while age-1 threadfin shad, American shad, and blueback herring each accounted for 8,9, and 4%, respectively (Table 5).

Table 5. Estimated production (P, in kg/ha) of threadfin shad (TFS), American shad (AMS), and blueback herring (BLH) in lakes Marion and Moultrie, SC, in the period August 7 through December 12, 2013. Weight (Wt) is expressed in grams. G is the instantaneous rate of increase in weight and B is the estimated mean biomass (kg/ha) of each species during the study period. Calculation assumes no mortality.

Species	8/7 Wt	12/12 Wt	G	B	P
TFS, age-0	5.18	9.00	0.55	34.54	19.08
TFS, age-1	13.54	16.12	0.17	11.51	2.01
AMS	3.55	9.31	0.97	2.14	2.07
BLH	1.34	3.65	1.00	0.97	0.97

The method of production estimation used in this analysis is meant as a first approximation, as the method assumes that no mortality (or recruitment) occurs during the study period. Obviously, mortality is occurring. In 2014, we will standardize gill net sets so that effort through the season is constant and an Allen curve can be generated, providing a more robust estimate of production.

The estimated, mean standing crop of 51 kg/ha in 2013 was considerably less than an estimate of 124 kg/ha obtained in October 2010 (N=4 transects). It is not known whether this level

of difference is normal for the system; future studies will help to understand this. The possibility exists that spatial variability of fishes may warrant a larger sample size to obtain a more precise estimate. The variability within a transect will be assessed in the following year to get an initial handle on whether sampling intensity is a substantial issue.

Recommendations

1. Continue hydroacoustic sampling in 2014, modifying sampling months to July through November.
2. Maintain constant gill netting effort in 2014, one surface and one mid-water so that better estimates of production can be made.
3. Incorporate the new estimates into system wide food web analysis conducted by the Santee-Cooper comprehensive study group.
4. Assess the variability of fishes within sampling transects to define whether current sampling effort is sufficient to obtain precise estimates.
5. Obtain additional training in Echoview, the software used to analyze the hydroacoustic results.

Job Title: Distribution of striped bass in J. Strom Thurmond Reservoir, South Carolina-Georgia, in relation to pump storage operation and hypolimnetic oxygenation

Period Covered July 1, 2013 – June 30, 2014

Summary

During 2014 34 striped bass *Morone saxatilis* and 11 hybrid striped bass *Morone saxatilis* x *Morone chrysops* collected from four tributaries to Thurmond Reservoir were implanted with acoustic transmitters. One hundred sixty-nine (169) striped bass have been successfully implanted since the study began in 2010. Implanted striped bass were detected by 64 different receivers stationed throughout the reservoir and were manually tracked on 39 dates. Twenty-nine percent (29%) of implanted striped bass appeared to be alive at the end of 2014, 15% of fish have expired transmitters, 41% have been harvested or assumed harvested, and the remaining fish have either died (9%) or are missing (5%). The Russell Tailrace and the oxygenated area of the lower reservoir were important habitats for striped bass during August 2010 - 2014 with all fish occupying one of those habitats during August of each year.

Introduction

J. Strom Thurmond (Thurmond) Reservoir supports a popular recreational striped bass fishery. Striped bass production at Thurmond is largely due to suitable habitat provided by artificially oxygenated, hypolimnetic releases from Richard B. Russell (Russell) Dam, that provide cool well oxygenated water in the tailrace and upper portions of Thurmond Reservoir during summer.

During 2011 Russell Dam commenced expanded pump-storage operations which could result in warmer tailrace temperatures below Russell Dam, possibly reducing suitable habitat for some species of fish. Given the unsuitable striped bass habitat throughout most of the reservoir during

summer the loss of the refuge in the Russell tailrace and upper Thurmond could have a negative impact on the striped bass fishery. To mitigate for the potential loss of striped bass habitat in the Russell tailrace and upper Thurmond, the USACE installed an oxygen injection system in the lower portion of Thurmond near Modoc, SC to provide striped bass habitat.

It is unknown how striped bass will utilize the potential reduction of habitat in the Russell tailrace and upper Thurmond or the new artificially oxygenated area in the lower reservoir. Considerable expense has been expended in the development and installation of the new oxygen injection system and it is important to document the extent of striped bass use of the newly-created habitat. Information on the seasonal distribution of striped bass after project implementation will be important for successful management of the striped bass fishery in Thurmond Reservoir.

Materials and Methods

The study will monitor the seasonal movement of adult striped bass in Thurmond Reservoir. Specifically monitoring their seasonal use of the current summer refuge area in the upper reaches of Thurmond and the Russell Tailrace as well as the enhanced area below Modoc, SC. In spring of 2010, 2011, and 2012, striped bass were collected from the Russell Tailrace and at least two major tributaries (e.g., Little River, GA and Little River, SC) and surgically implanted with individually coded temperature sensing acoustic transmitters. During spring of 2013 and 2014 striped bass were collected from at least three tributaries; no fish were collected from the tailrace, and implanted with transmitters. Hybrid striped bass were collected from up to three tributaries during 2013 and 2014 and implanted with transmitters. Two different transmitters manufactured by *Sonotronics* were used based on fish length. A high powered long-range transmitter (Model CHP-87-L) expected to last 18 months was implanted in striped bass > 575 mm TL and a less powerful transmitter (Model CTT-83-

3) expected to last 36 months was implanted in striped bass > 480 mm TL. To facilitate the return of transmitters from harvested fish external reward tags (Hallprint Pty Ltd., Victor Harbor, South Australia) were inserted into most striped bass implanted during 2013 and 2014.

An array of remote acoustic receivers (SUR-3BT, *Sonotronics Inc.*) was used to collect movement data from transmitter implanted fish (Figure 1). Receivers were positioned throughout the mainstem reservoir with expanded arrays in the tailrace and oxygen injected area to achieve continuous coverage of the Savannah River channel in those areas. Additional location data was collected with a hand held ultrasonic receiver (USR-08, *Sonotronics Inc.*) to identify other potential refuges and locate missing fish. Temperature and oxygen profiles at 1-m depth intervals were collected monthly during the summer study period at a series of fixed stations.

We considered four possible fates for transmitter implanted fish in J. Strom Thurmond Reservoir. Striped bass could be, alive in the fishery until the conclusion of the study (or transmitter expiration), harvested, missing, or die of natural causes. During 2013 we posted signs at major access points, and issued press releases to inform anglers of the ongoing telemetry study. Signs and press releases advised anglers that a \$50.00 reward would be given for returning transmitters from harvested fish. Fish were determined to be harvested when an angler returned a transmitter from a captured fish, or were assumed harvested when a fish went missing from an area with overlapping receiver coverage, and were not detected in subsequent manual searches. Fish lost from the fishery were either confirmed as dead by lack of movement during manual searches or simply classified as missing when they were no longer located at receiver stations or during manual searches. Due to the extensive receiver network it was unlikely that fish classified as missing were at large and simply undetected so ultimately they were lost from the fishery by harvest or natural mortality.

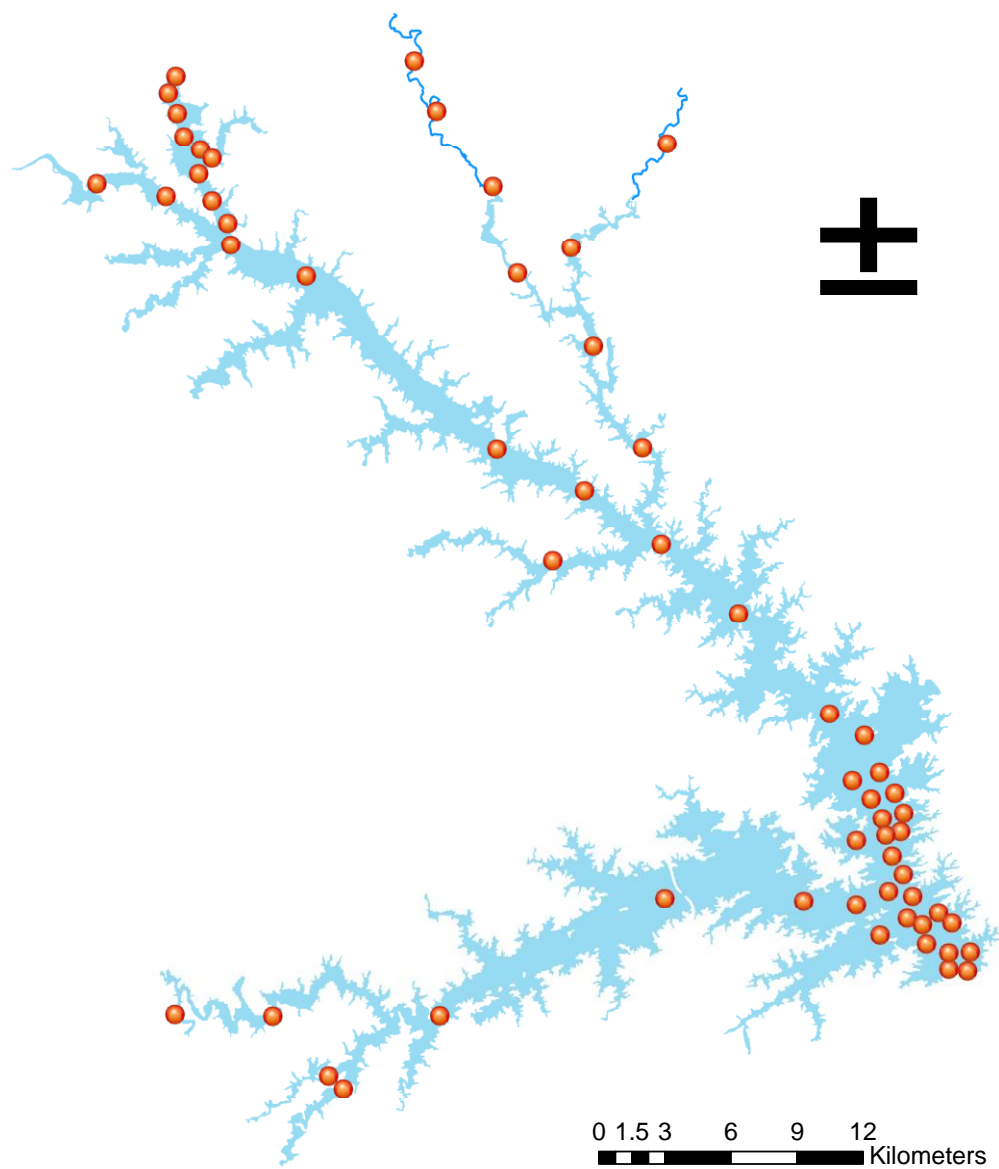


Figure 1. Acoustic receiver locations in J. Strom Thurmond Reservoir SC-GA, during 2010 -2014.

To evaluate striped bass use of the newly created summer habitat, due to oxygenation, in the lower reservoir the average position of each transmitter-implanted striped bass was calculated for August of each year.

Results

Thirty-four (34) striped bass (mean TL = 795 mm; range 525 – 1160 mm TL) collected from four tributaries to Thurmond Reservoir were implanted with acoustic transmitters between 24 February 2014 and 10 April 2014. Thirty-three (33) of those fish also received an external reward tag. Since April 2010 a total of 185 striped bass collected from Thurmond Reservoir and its tributaries have been implanted with transmitters. Eleven (11) hybrid Striped Bass (mean TL = 562 mm; range 492 – 655 mm TL) collected from three tributaries to Thurmond Reservoir were implanted with transmitters between 2 February and 10 April 2014. Since April 2013 a total of 25 hybrid striped bass have been implanted with transmitters.

Submersible acoustic receivers at up to 64 different sites were used to collect striped bass movement information during 2010 - 2014 (Figure 1). Striped bass and hybrid striped bass implanted with transmitters were manually tracked on 39 dates during 2014.

There have been roughly 8.4 million detections at the receiver locations. The average number of detections at receiver locations for striped bass known to survive transmitter implantation was 46,476 through August 2014 (Table 1). During manual tracking events 143 different striped bass were located at least once with a total of 449 detections. The average number of detections at receiver locations for hybrid striped bass known to survive transmitter implantation was 21,434 (Range; 445 – 85,123) through August 2014. During manual tracking events 11 different hybrid striped bass were located at least once.

Table 1. Tagging year, number of successfully implanted striped bass, mean TL (mm), Mean number of days tracked, mean number of detections at receiver stations and total number of manual tracking detections for transmitter implanted striped bass in Thurmond Reservoir, SC-GA through August 2014. Range for means given in parentheses. Table does not include 9 fish that were suspected to die due to tagging and seven fish whose fates could not be determined.

Year	N	Mean TL	Days Tracked	Receiver	Manual
2010	33	737 (480 - 1,400)	492 (0 – 1,258)	67,578 (5 – 239,457)	139
2011	31	741 (550 – 1,300)	376 (4 – 1,051)	41,592 (990 – 204,559)	77
2012	33	729 (487 – 1,025)	415 (3 - 921)	58,588 (188 – 210,608)	72
2013	38	826 (627 – 1,155)	323 (11 - 574)	41,735 (162 – 121,381)	75
2014	34	795 (525 – 1,160)	165 (44 - 212)	23,990 (763 – 62,348)	86
Total	169	768 (480 -1,400)	352 (0 – 1,258)	46,476 (5 -239,457)	449

At the conclusion of 2014, 29% of successfully implanted striped bass were assumed to be alive, 41% were harvested or assumed to have been harvested, 9% of fish had died, and the remaining fish either had expired transmitters or were missing (Figure 2). Striped bass tagged during 2010 – 2012 have displayed consistent mortality among tagging years. Mean survival for fish tagged during those three years was 35% (range, 32% - 36%) and mean mortality was 65% (range, 64% - 68%). The vast majority (82%) of that mortality has been due to reported or inferred harvest. Natural mortality appears to be low for striped bass in Thurmond Reservoir.

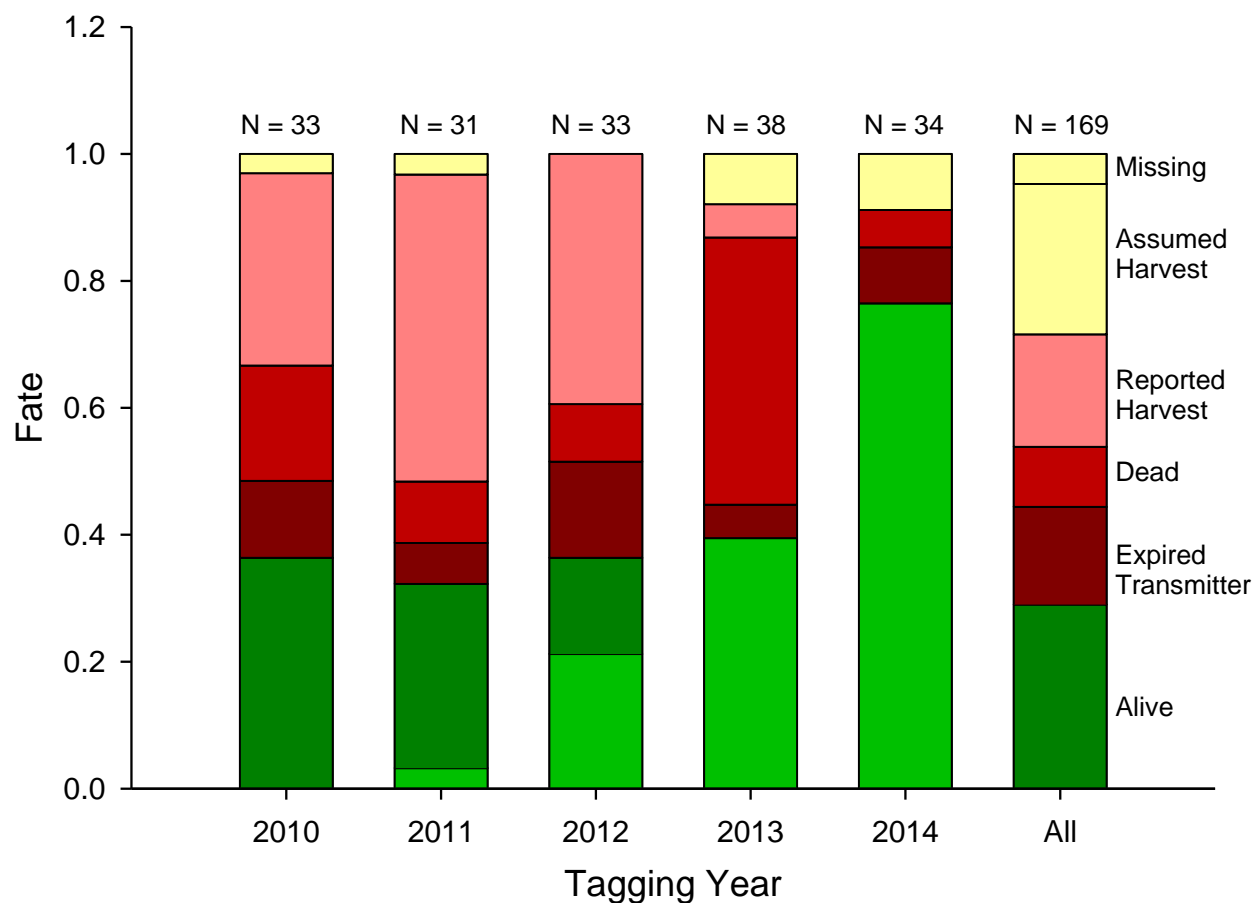


Figure 2. Proportion of striped bass in each fate category for striped bass implanted with transmitters in Thurmond Reservoir during 2010 - 2014.

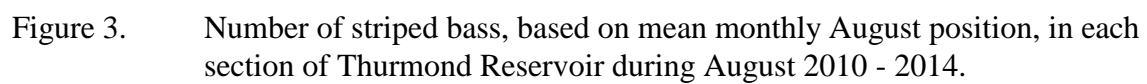
At the conclusion of 2014, 37% of successfully implanted hybrid striped bass were assumed to be alive, 26% were harvested or assumed to have been harvested, 32% of fish were missing, and one fish emigrated from the study area passing through the turbines at Thurmond Dam down into the Thurmond Tailrace (Table 2). Tagging mortality of hybrid striped bass was high, with 6 of the 25 fish implanted assumed to have died due to tagging.

Table 2. Fate of hybrid striped bass implanted during 2013 and 2014 in J. Strom Thurmond Reservoir, SC-GA.

Year				Assumed		Tagging
Implanted	Alive	Emigrated	Harvested	Harvested	Missing	Mortality
2013	2	1	1	3	3	4
2014	5	0	1	0	3	2
Total	7	1	2	3	6	6

Since oxygenation striped bass use of the lower reservoir during summer (August) has increased each year. During August 2010, before oxygenation, only two implanted striped bass used the lower reservoir; however, there has been a steady increase in the number of implanted striped using the lower reservoir since oxygenation began in 2011 with 29 implanted striped bass using the lower reservoir in 2014 (Figure 3).

Water temperature and dissolved oxygen profiles were collected from 10 sites located longitudinally from Thurmond Dam to Russell Dam during July, August, September, and October of 2013 and May and June of 2014. Temperature and dissolved oxygen profiles were also collected at 16 fish locations during the study period. Water quality profiles have not been summarized.



Discussion

Location data downloaded from receivers during 2014 has been incorporated into an Access database; however, rigorous analysis of those data has not been completed. cursory examination of the data does show the importance of the Russell Tailrace and oxygenated area near Modoc as a summer habitat for striped bass. All fish have had their average monthly location during August located in the tailrace or oxygenated area except during 2012 when two fish moved between the two habitats during late August (Figure 2). Although, the proportion of fish utilizing the lower reservoir during August has increased dramatically some of that increase is likely due to the propensity for fish tagged in the various tributaries to utilize different summer habitats. For example, the majority of fish implanted in the Broad River, and all fish implanted in the tailrace and followed for at least one summer utilized the tailrace during summer. Fish implanted in Little River, South Carolina used the tailrace and lower reservoir in nearly equal proportions while fish implanted in Little River, Georgia were more likely to utilize the lower reservoir than tailrace during summer. The decrease in the proportion of fish that utilize the tailrace during summer is partially due to implanting fewer fish from the tailrace each year. Removing striped bass captured from the tailrace shows a less dramatic, but consistent increase in the proportion of fish using the lower reservoir during summer (Figure 4). The proportion of fish utilizing the lower reservoir during summer has increased each year from 22% during 2010, before oxygenation, to 55% during 2014.

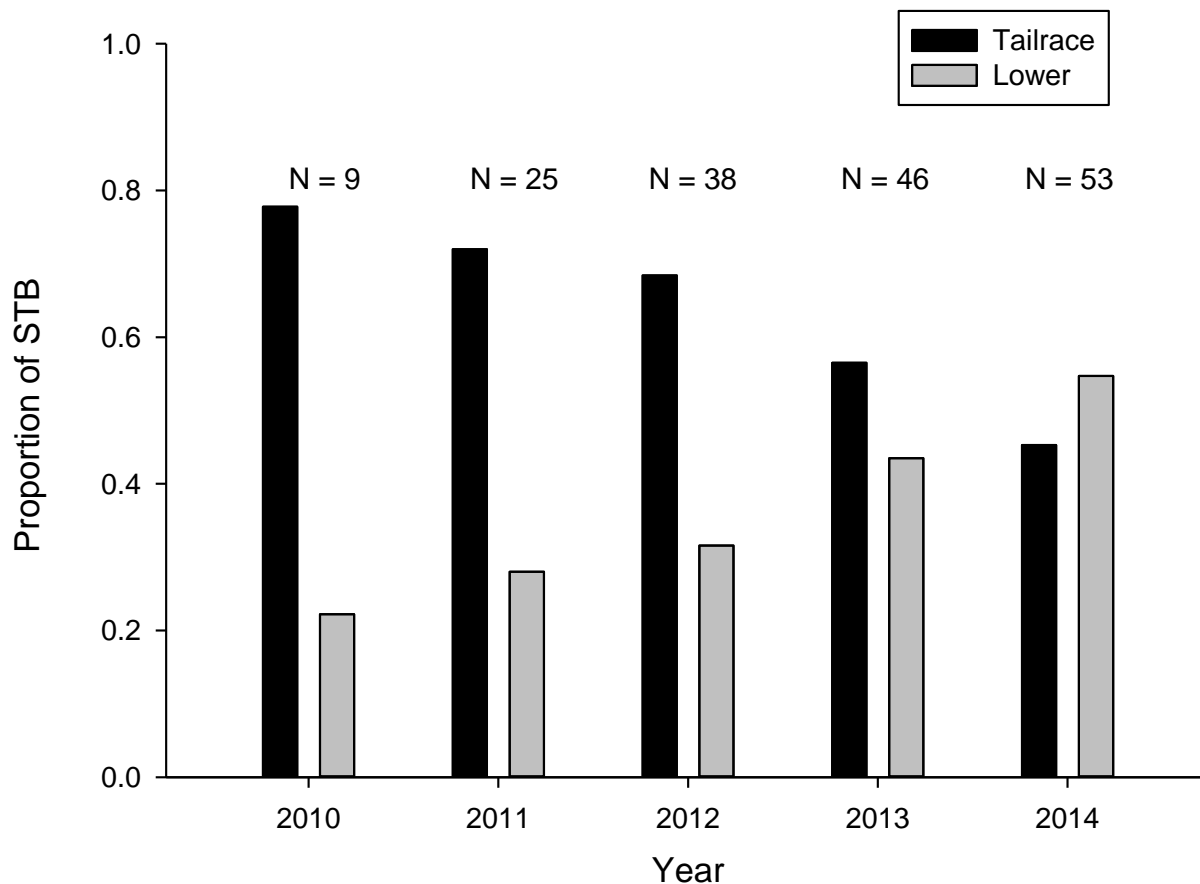


Figure 4. Proportion of striped bass tagged outside the Russell Tailrace utilizing the lower reservoir or Russell Tailrace during August 2010 - 2014.

Striped bass in Thurmond exhibit strong site fidelity to their summer habitat. Fifty-eight (58) fish have been tracked for at least two summers (3 for four summers and 18 for three summers) and nearly all of those fish have used the same habitat each August. Two fish followed through summer 2014 may have switched their August habitat, one fish using the tailrace in 2013 appears to have used the lower reservoir in 2014, and one fish that used the lower reservoir during 2013 moved to the tailrace during 2014. Whether these are anomalous observations or an actual switch in summer habitat will not be known until fall 2014 data is fully processed.

During 2013 and 2014 we attached external reward tags to implanted striped bass to increase reporting rates of harvested striped bass and to validate assumptions about how we categorize the fate (i.e., “Alive”, “Dead”, or “Harvested”) of striped bass. The external tags were effective in increasing reporting rates and validated assumptions about how we categorize the fate of implanted fish. During 2010 – 2012 we had poor transmitter return rates; although we categorized at least 16 fish as harvested from each of the 2010 – 2012 implantations the majority (>76%) of those fates were based on location information that indicated that fish were removed from the lake and not from harvest reports. For the 2013 implanted fish, which had external reward tags, 16 fish were reported as harvested and only 2 fish were classified as harvested based on location history and absence during manual searches. There is qualitative agreement between the percentage of fish categorized as harvested (mean = 52%) from each tagging year (2010 -2012) before the use of external reward tags with reported harvest (47%) during 2013 after the use of external reward tags (Figure 2).

We have had comparatively poor success implanting hybrid striped bass. Tagging mortality for striped bass has been low (5%); however, tagging mortality of hybrid striped bass has been much higher (24%). The higher tagging mortality rates of hybrid striped bass may be related to fish size, and/or water temperatures at the time of tagging. Hybrid striped bass are generally much smaller than striped bass, and are typically tagged later in the spring after water temperatures have warmed.

Recommendations

Outside funding for the field component of this study is scheduled to end December 2014; with a final report due June 2015. With 49 striped bass, and 7 hybrid striped bass, at large with active transmitters it is recommended that we continue to monitor, with reduced surveillance, their movements through at least May 2015. Monitoring fish movements through May 2015 will allow us

to calculate mortality estimates from two full years with the benefit or external reward tags and capture mortality during the spring season which has the highest exploitation rates.

Job Title: Redbreast Stocking Evaluation – Edisto River

Period Covered July 1, 2013 – June 30, 2014

Summary

An evaluation of the stocking of redbreast sunfish *Lepomis auritus* on the Edisto River was initiated in 2010 and has continued. In 2013, 287,943 redbreast were produced (2013 year class), immersion-marked in oxytetracycline (OTC), and stocked in a prescribed zone of the Edisto River main stem. Mark evaluations on N=30 known marked fish from this year class were completed and OTC marks were confirmed on all fish examined. These included representatives from three separate mark events. Because marks were variable, and some were classified as faint, a blind set of otoliths from known marked and unmarked fish from the same 2013 year class was produced and evaluated. Marked and unmarked fish were identified with 100% accuracy by an experienced reader. We plan to assess the contribution of hatchery stocked fish from the 2013 year class to the receiving fishery with collections of adults from the wild in Fall 2014. This will represent the second year class assessed for this study. A 2014 year class will also be produced, marked, and stocked.

Introduction

Redbreast sunfish is a much sought after sport fish on the Edisto River. This is evidenced in collections made in 2004 that spanned a very high water event. Those collections suggest that once hydrologic conditions normalized, allowing for greater river access and angling, larger fish were quickly exploited and removed (Bulak 2005). The annual stocking of redbreast sunfish began in Edisto River in 1995. This was in response to public concerns that introduced flathead catfish *Pylodictis olivaris* were negatively impacting the popular fishery. Records show approximately 13.7

million redbreast stocked in the river since 1995, with annual stocking ranging from 0.45-2.2 million.

The supplemental stocking of redbreast sunfish in Edisto River has never been evaluated. Collections of microtagged redbreast sunfish that were stocked in Little Pee Dee River from 1990 – 1992 suggested minimal contribution, though further sampling was recommended before drawing conclusions from the available data (Crochet and Sample 1993). Genetic survey of redbreast sunfish populations across five South Carolina drainages indicated Edisto river redbreast were markedly less diverse than redbreast populations from other drainages (Leitner 2006). This could be a result of lost diversity in the former hatchery population and its impact on the receiving population in the river, or could be an indication of bottleneck events occurring in the wild. To best manage this resource, we need a basic understanding of whether supplemental stocking is contributing to the redbreast sunfish population and fishery of the Edisto River. In the last year 287,943 redbreast were produced (2013 year class), immersion-marked in oxytetracycline (OTC), and stocked in a prescribed zone of the Edisto River main stem. A mark evaluation of known marked fish from this year class was conducted and is reported on here.

Materials and Methods

Known marked redbreast sunfish fingerlings from three mark events in 2013, and known unmarked fish from the same year class were grown out for approximately six months, and then provided to this lab for mark evaluation. Otoliths from these fish were processed according to standard procedures for OTC mark evaluation.

Initially N=10 known marked fish were evaluated from each mark event. Following this evaluation, a blind set of otoliths including both marked and unmarked individuals was produced and

evaluated. Because growth varied among the four grow out groups, fish were selected for use in the blind set based on size. This helped ensure that the set was truly blind, and individual groups would not be identifiable by differences in growth apparent in the otoliths.

Results and Discussion

OTC marks were visible on the otoliths from all known marked fish (N=30) initially evaluated. Marks were variable however and ranged in quality from bright to faint. The presence of faint marks among known marked fish led us to develop the blind set with known unmarked fish included. This is to further test our ability to identify marked fish collected from the wild.

Fish included in the blind set ranged in size from 60 – 75 mm tl. Mean size across the four groups evaluated is presented in Table 1. Marked and unmarked fish were correctly identified 100% of the time by an experienced reader. Based on the positive mark evaluation results we will move forward with assessment of the 2013 year class in the wild. Fish will be collected from prescribed zones of the Edisto River at age 1+ and contribution of hatchery stocked fish to the year class will be estimated.

Table 1. Total length (tl) of 2010 year class known marked and unmarked redbreast sunfish used in blind set for oxytetracycline mark evaluation.

Group	N	Mean tl (mm)	Range	Standard Deviation
Mark Vat 7	5	67.2	62 - 71	3.7
Mark Vat 8	5	63.8	60 - 72	4.8
Mark Vat 14	8	68.7	65 - 70	1.8
Unmarked Vat 1	20	65.9	60 - 75	4.3

The 2013 year class will be the second year class we have collected for the assessment of hatchery contribution. The first was from 2010, and at age 1+ hatchery fish comprised 9% of the total redbreast collected. Difficulties in marking and grow out precluded our assessment of fish stocked in 2011 and 2012. This study will continue and in 2014 an additional year class of redbreast will be produced, marked and stocked.

Recommendations

Continue study. Collect and assess the 2013 year class from the wild. Mark and stock a 2014 year class of redbreast sunfish, following in place protocols. Ensure an extended grow out is allowed for a sufficient sample of fish from each mark event, and of known unmarked fish from the same year class. Following grow out, complete mark evaluations of the 2014 year class with a blind set of known marked and unmarked fish. Repeat marking and stocking assessment until a minimum of 3 year class stocking evaluations are completed.

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Job Title: Trophic resources for larval fish in Lake Marion

Period Covered July 1, 2013 – June 30, 2014

Summary

In 2013-2014 we focused on integrating results from analyses of various processes in the main basin of upper Lake Marion to understand processes affecting abundances of zooplankton and phytoplankton. We use these results to consider whether larvae striped bass *Morone saxatilis* and other ichthyoplankton are subject to competition for food resources; further evaluation is contingent on refinement of estimates of planktivorous fish in the region. We also completed processing and analysis of benthic samples from Lake Moultrie and additional samples from Lake Marion; these results develop our understanding of longitudinal variation in this system.

Introduction

In 2008, the South Carolina Department of Natural Resources (SCDNR) re-convened the Santee-Cooper Comprehensive Study Group to provide an update and overview of current conditions in the system and to guide and promote development of a scientific basis for management decisions about aquatic resources within the Santee-Cooper basin. The work reported here is part of the final phase of studies directed toward developing process-based models of food resources and other factors that may affect recruitment of key resident and anadromous fish species in the Santee-Cooper system.

These species, as identified by the Study Group, include striped bass, American shad *Alosa sapidissima*, blueback herring *Alosa aestivalis*, threadfin shad *Dorosoma petenense*, and white perch *Morone americana*. These key species have overlapping spawning seasons (April to June); they share nursery areas in upper Lake Marion; and, in their larval stages, they feed on zooplankton.

Our general objectives were to assess current conditions in the lake, quantify trophic structure, and to model and evaluate processes that may influence trophic interactions, with particular attention to the key fish species. A specific objective from the Study Group was to evaluate whether low zooplankton abundance, resulting in competition for food, may limit recruitment of key fish species. We focused on upper Lake Marion, because of its importance as a nursery.

Materials and Methods

Assessment of importance of competition to success of ichthyoplankton in upper Lake Marion

The main field results and models used in this synthesis have been described in previous reports. The food web in upper Lake Marion is dominated in biomass by the Asiatic clam, *Corbicula fluminea*, and other molluscs (Taylor, 2012). We built a model for zooplankton dynamics to evaluate potential impacts of hydrologic processes, predation by larval fish, and by pelagic young-of-year and adult planktivorous fish (Taylor, 2011 and 2012). We also built a model for phytoplankton dynamics to evaluate potential impacts of hydrologic processes and consumption by *Corbicula* (Taylor, 2013).

Further analysis of zooplankton field data for 2012 gave us improved estimates of birth rates, which were used in the new applications of the zooplankton model. The basin in the phytoplankton dynamics model was expanded from one to three linearly connected compartments for new simulations.

Benthos in lower Lake Marion and Lake Moultrie

Working cooperatively with Santee-Cooper staff, we sampled the benthos of Lake Moultrie and lower Lake Marion. The sampling program in Lake Moultrie (25 samples on five transects) was designed to provide a comprehensive initial assessment of the benthos. The sampling program in lower Lake Marion was designed to augment sample coverage in 2010, adding two transects across

the lake and extending transects into two of the coves. Samples were collected with a mini Ponar dredge (6-inch by 6-inch sample surface area). Invertebrates were separated from the sediment on a 500-micron mesh sieve. Additional samples at each location were collected for analysis of sediment texture and organic carbon content. Dry biomass of benthic animal tissue was estimated from published regressions.

Results and Discussion

Assessment of importance of competition to success of ichthyoplankton in the main basin of Upper Lake Marion

Growth and survival of larval fish depends on an adequate supply of zooplankton. Based on extensive field studies in Lake Thurmond, Betsill and Van Den Avyle (1997) concluded that growth and survival larval threadfin shad diminished at zooplankton abundances below a threshold around 200-300 animals/L. Chick and Van Den Avyle (1997) inferred from feeding experiments that larval striped bass feeding on zooplankton from Lake Marion would require around 100 animals/L.

Relative to these thresholds, spring abundances of zooplankton in the main basin of Lake Marion have been generally low during our studies. Mean total abundance (all rotifers and microcrustaceans combined) was <100 animals/L on all sampled dates in April and May in 2009 and 2012 (see Taylor, 2012), and spring 2014 samples are yielding similar results.

Figure 1 illustrates components of the food web in spring, including connections we have examined to understand processes that may limit resources available to the ichthyoplankton spring. Table 1 summarizes our current evaluations of the interactions.

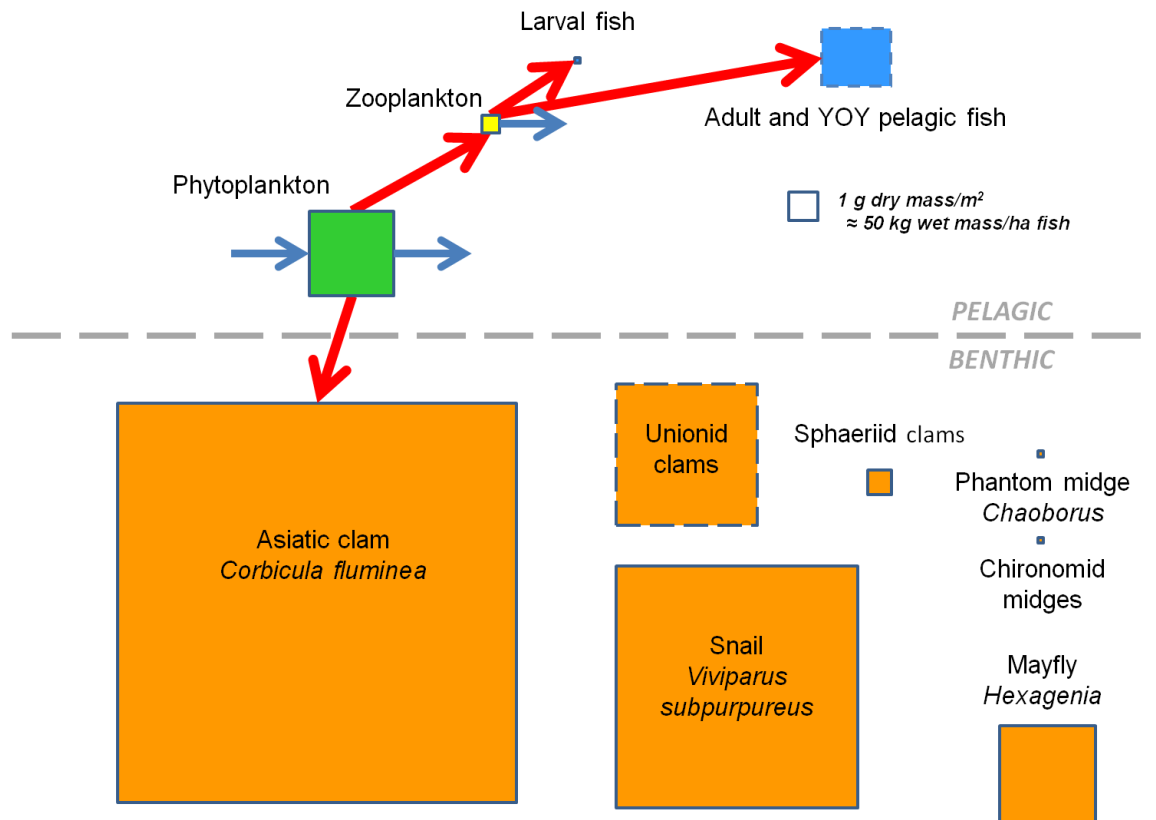


Figure 1. Biomass of benthos in upper, middle, and lower main basins of Lake Marion and in Lake Moultrie. Pie chart areas are proportional to relative biomass among regions. Data for Lake Marion in 2009-2010 and Lake Moultrie in 2013 are shown.

Table 1. Main interactions among components of food web in upper Lake Marion in spring.

<i>Component</i>	<i>Interactions</i>
Phytoplankton	Consumption by zooplankton is negligible Modeled consumption by <i>Corbicula</i> , if feeding mainly on phytoplankton, is substantial Import from river and uplake regions may be substantial Phytoplankton dynamics is responsive to discharge from the river
Benthos	Feeding by <i>Corbicula</i> potentially transfers large quantity of material from pelagic to benthic habitat Excess consumption by <i>Corbicula</i> may supplement diets of other benthic consumers, including <i>Hexagenia</i>
Zooplankton	Import from river and uplake regions is negligible Rotifer abundance is correlated with phytoplankton abundance; cladoceran fecundities suggest some effect Predation by planktivorous larval fish is negligible Low populations of planktivorous young-of-year and pelagic fish could deplete zooplankton
Planktivorous larval fish	Abundance of zooplankton is often low, relative to densities reported to sustain maximum growth and survival
Pelagic YOY and adult fish	Spring zooplankton populations are insufficient to support even low populations of planktivorous fish

The largest component of the biomass in the food web, and potentially the largest consumer of phytoplankton, is the Asiatic clam, *Corbicula fluminea*. Simulations results (Table 2) indicate that the clam population suppresses phytoplankton production and may divert a substantial proportion of phytoplankton production from pelagic to benthic habitat. One surprising result was the importance of imported phytoplankton production to this system. The estimates of algal concentrations in the Santee River that we used to set parameters for the model were made in 1989-1991; DHEC water quality programs routinely measure of chlorophyll in lakes, but not in rivers. At our request, Santee Cooper began sampling chlorophyll a in the Santee River this summer.

Table 2. Simulated spring phytoplankton production in upper Lake Marion. Simulation uses a 3-compartment model of upper main basin. Ranges of results for 2-month simulations with various parameters are shown; 2009 daily discharge values for Santee River were used in all simulations.

<i>Process</i>	<i>Average phytoplankton production for April-May (metric tons dry mass/day)</i>
Import from Santee River	10-20
Influent chlorophyll concentration $A_{river} = 2$ or $4 \mu\text{g chl a/L}$	
Algal production	1-60
Production rate coefficient $p = 0.3$ or $0.4/\text{day}$	
Consumption by clam	7-15
Algal dry biomass as percentage of clam dry biomass: $C = 0.5$ or $1\%/\text{day}$	
Export to middle Lake Marion	2-79

Corbicula would affect larval fish indirectly, if a reduction in production of phytoplankton limited production of zooplankton. Abundances of rotifers, but not of cladocerans or copepods,

were strongly correlated with chlorophyll a in 2009 (comparable chlorophyll data were not available in subsequent years). The dominant cladoceran in most of the spring samples for both 2009 and 2012 was *Bosmina longirostris*, a species which can feed efficiently at lower phytoplankton concentrations than can some other cladocerans (DeMott, 1982). Egg-ratio based estimates of birth rates for 2012 indicate that its productivity was reduced (birth rates of 0.1-0.2/day) but not completely suppressed on some dates in spring; rates ranged as high as 0.4/day in mid-June.

The largest unknown factor in the model for zooplankton dynamics remains the magnitude of predation by pelagic adult and young-of-year fish. Given the relatively high spring flushing rates of the upper basin, the zooplankton populations would not sustain consumption by even a modest population by fish (Figure 2).

Threadfin shad is one of the dominant pelagic fish in this system. Its diet however, appears to be highly variable, and it often feeds mainly as a detritivore (e.g., Hendricks and Noble, 1997). In Lake Jordan, North Carolina, Jackson et al. (1990) found that both threadfin and gizzard shad were detritivores, except during “a brief period early in the growing season coincidental with peak zooplankton densities.” In Trinidad Lake, Texas, threadfin shad were also primarily detritivores. At nearshore sites in upper and middle Lake Marion, young-of-year threadfin shad (Bettinger, 2013) fed extensively on algae and unidentifiable benthic material (the source inferred by presence of sand), as well as rotifers and microcrustaceans.

Our current assessment is that the resource base for larval fish in the upper main basin is controlled primarily by phytoplankton abundances and by advective losses. Competition between larval fish and adult threadfin shad may occur opportunistically. A better assessment awaits spring 2014 and 2015 data on pelagic fish composition and abundance.

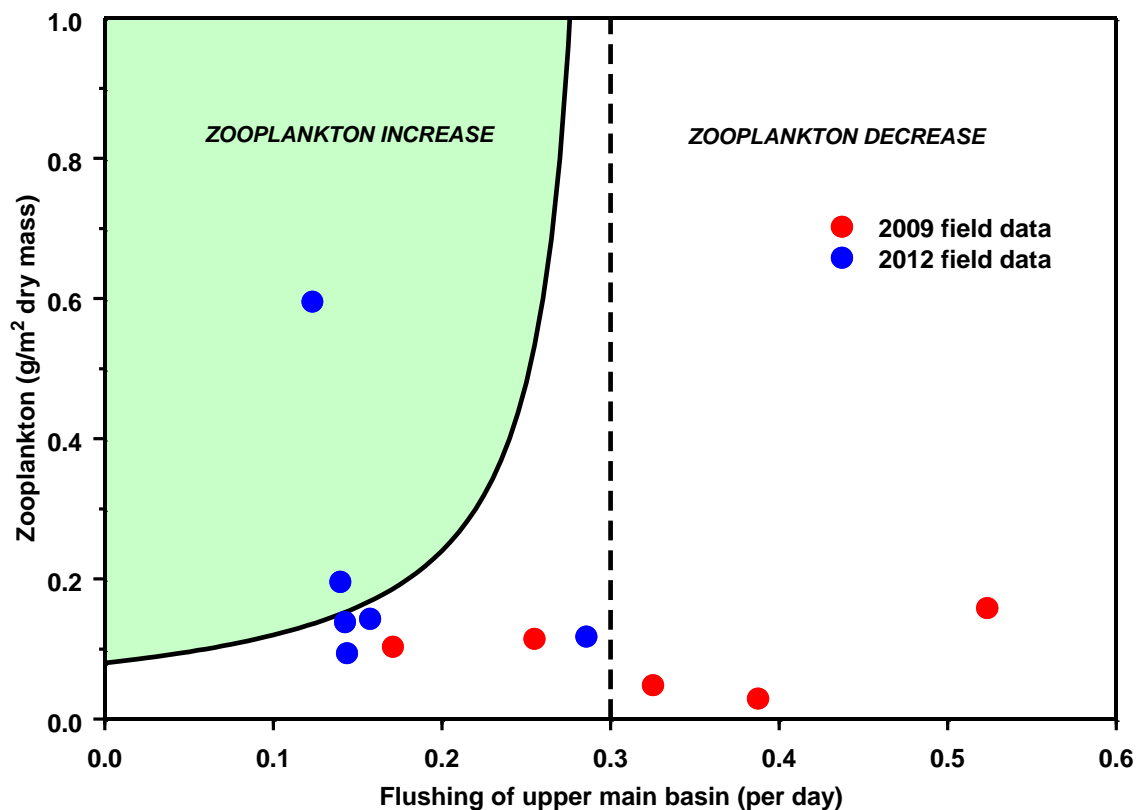


Figure 2. Potential impact of fish predation on zooplankton dynamics. Depending on the flushing rate of the basin and abundance of zooplankton, the zooplankton population will increase (green region) or decrease (white region). Fish biomass is modeled at 12 kg/ha (10% of estimate from fall 2010 hydroacoustic survey); consumption per unit biomass is based on Stewart and Binkowski's (1986) YOY alewife model. Zooplankton birth rate is modeled at 0.3/day.

Benthos in lower Lake Marion and Lake Moultrie

The abundance and biomass of the benthos in lower Lake Marion in 2013 were generally consistent with 2010 samples, showing a paucity of mollusks and an absence of the burrowing mayfly *Hexagenia limbata*, even in the 2-6 m depth range that was poorly represented in the 2010 samples (Table 3). One difference between the 2010 and 2013 samples for lower Lake Marion is the greater relative abundance of crustaceans in the 2013 samples. This difference may reflect a temporal change in the benthic community or differences in the set of stations sampled.

Sediments of Lake Moultrie were sand-dominated, and the average total organic carbon content was 0.8%. In contrast, sediments of Lake Marion were silt-dominated, and average total organic carbon was 2.5% (2009-2010 data for all three regions combined).

Biomass of the benthos in Lake Moultrie was similar to that of lower Lake Marion (Figure 3). The Asiatic clam dominated biomass. We speculate that the low biomass in Lake Moultrie reflects both lower planktonic productivity and a diminished supply of allochthonous material. Material transported into Lake Marion by the Santee River is probably largely removed by biological processes before it can reach Lake Moultrie.

Recommendations

During 2015 we will incorporate results from 2014 and 2015 fish studies into this synthesis, and we will complete a final report on the benthos.

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Table 3. Abundance and biomass of benthic invertebrates sampled in 2013 in lower Lake Marion and Lake Moultrie. Biomass was not estimated for some sparsely abundant or small taxa.

<i>Taxon</i>	<i>Lower Lake Marion (n=25 samples)</i>		<i>Lake Moultrie (n=25 samples)</i>	
	<i>Abundance (#/m²)</i>	<i>Biomass (g/m²)</i>	<i>Abundance (#/m²)</i>	<i>Biomass (g/m²)</i>
BIVALVES	255	7.6	255	9.9
Corbiculidae: <i>Corbicula fluminea</i>	81	6.4	166	9.8
Sphaeriidae	173	0.1	88	0.1
GASTROPODS	5	0.6	2	0.0
Viviparidae: <i>Viviparus subpurpureus</i>	5	0.6	2	0.0
INSECTS	596	0.0	146	0.0
Coleoptera	2		0	
Diptera: Chaoboridae: <i>Chaoborus punctipennis</i>	142	0.0	35	0.0
Chironomidae	442	0.0	85	0.0
Ephemeroptera: Caenidae: <i>Caenis</i>	5	-	14	-
Odonata	0	-	5	-
Trichoptera	5	-	7	
CRUSTACEANS	360	0.7	194	0.4
Amphipoda	300	0.6	189	0.4
Copepoda: Cyclopoida	2	-	3	-
Isopoda	31	0.1	0	0.0
Ostracoda	28	0.1	2	0.0
TOTAL	1221	7.9	596	10.3

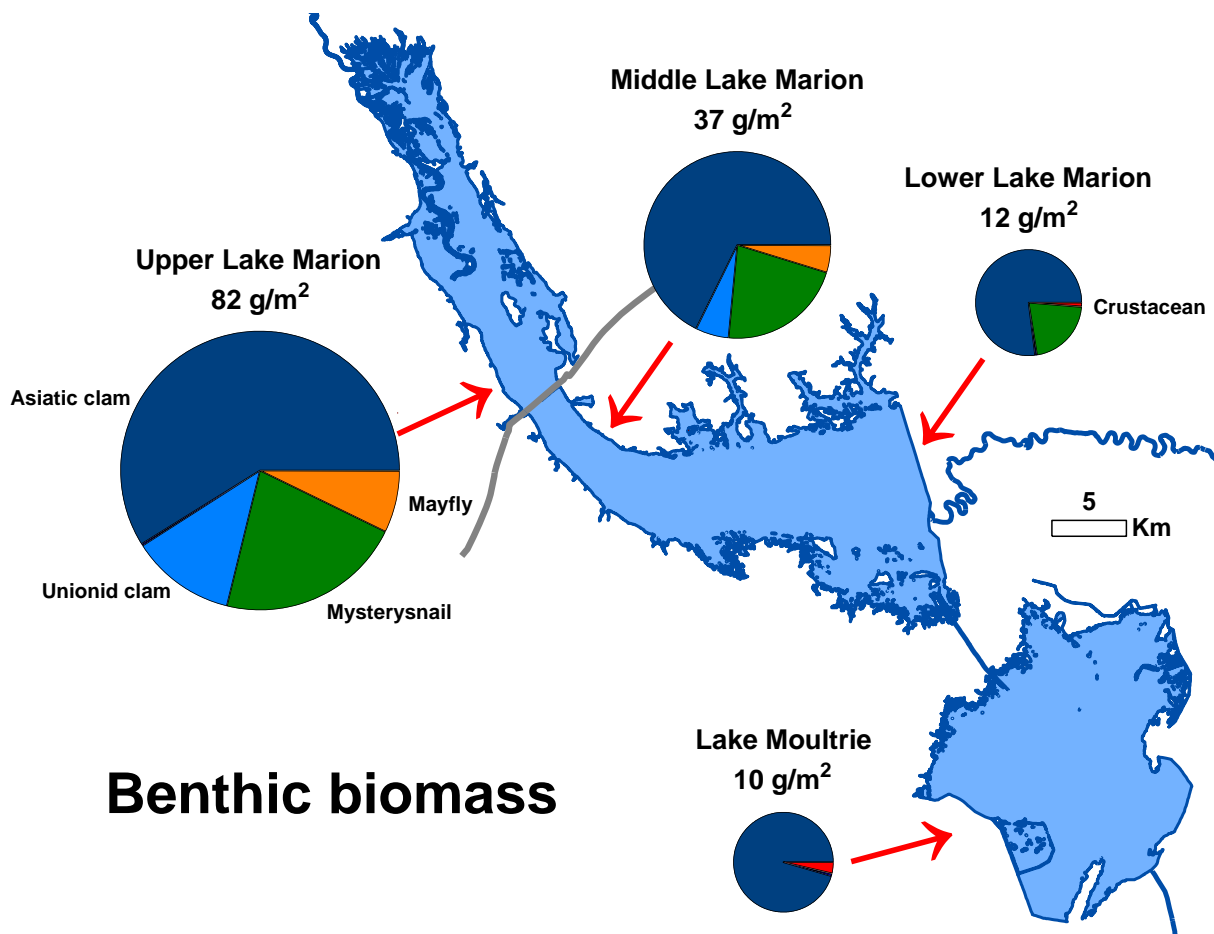


Figure 3. Biomass of benthos in upper, middle, and lower main basins of Lake Marion and in Lake Moultrie. Pie chart areas are proportional to relative biomass among regions. Data for Lake Marion in 2009-2010 and Lake Moultrie in 2013 are shown.

Job Title: Assessment of condition, growth, contribution to fish community, and diet of striped bass, white perch, and American shad young-of-the-year in the Santee-Cooper lakes, South Carolina

Period Covered July 1, 2013 – June 30, 2014

Summary

Standardized boat electrofishing was conducted at Lake Marion each year 2009 - 2013 to evaluate young-of-year (YOY) growth, condition, abundance and diet of key species. Data collected from Lake Moultrie during the same time period (2009 – 2013) and using the same collection methods was pooled with Lake Marion data to evaluate differences in growth, abundance and condition of key species between lakes. Striped bass *Morone saxatilis* YOY mean total length (TL mm) was higher in Lake Marion than Lake Moultrie and striped bass mean TL varied among years; however, “growth” during the study period was only different in 2008 when striped bass grew very quickly compared to other years. Mean TL of YOY white perch *Morone americana* and American shad *Alosa sapidissima* differed among years, but not lakes. Striped bass and white perch condition were higher in Lake Marion than Lake Moultrie and varied among years. American shad condition did not vary between lakes but did differ among years. Analysis of catch-per-unit-effort (CPUE) was restricted to Lake Marion where it varied among years for white perch and striped bass, but not for American shad.

We continued our evaluation of the diet of YOY striped bass, American shad and white perch. The stomach contents of 59 American shad collected from pelagic areas of Lake Marion and Lake Moultrie during 2013 were processed. Dry weights were generated for 24,980 prey items identified in the stomach contents of YOY fish. American shad collected from pelagic areas during

2013 had a more varied diet, and much greater consumption of micro crustaceans, than those collected from shoreline samples during 2009.

Introduction

‘Fingerling mortality’ of striped bass is a key issue for the Santee-Cooper striped bass stakeholders and it has been a key issue of the DNR for many years. Many hypotheses have been generated to define the causes of either good or poor recruitment in a given year. These hypotheses include, but are not limited to, reduction in the adult spawning stock, competition with resident and anadromous species, and reduced nutrient inflow due to drought. The Santee-Cooper Comprehensive study group of the DNR defined investigation of the ‘competition for resources’ hypotheses as its primary short-term goal. A strategy was needed to obtain key monitoring data on the species of interest. The objectives of this study are to, 1) Define growth and condition of key juvenile species, 2) describe the diet of each species and 3) define the relative abundance of each key species.

Materials and Methods

Growth, condition and abundance

Young-of-year (YOY) American shad, blueback herring *Alosa aestivalis*, threadfin shad *Dorosoma petenense*, white perch and striped bass were collected at least monthly from two Lake Marion sites with boat electrofishing gear during each summer 2009 -2012. During 2013 electrofishing was only conducted during September and October (Table 1). At each site night-time electrofishing was conducted for roughly 10 minutes at each of three transects, except for 2013 when only two standardized transects were sampled at each site. A third non-standard transect was conducted at “Big Water” to increase the sample size of YOY striped bass to evaluate the

contribution of wild and hatchery-stocked striped bass to the 2013 year class. We attempted to collect all YOY of the targeted species. Specimens were placed on ice and measured (TL, mm) and weighed (g) within 24 hours of collection.

Table 1. Year of sampling, beginning and ending date of sampling, number of transects sampled each year and electrofishing effort (h) during nighttime electrofishing at two sites on Lake Marion, SC during 2009 - 2013.

Year	Begin Date	End Date	Big Water		Indian Bluff		Total	
			Transects	Effort (h)	Transects	Effort (h)	Transects	Effort (h)
2009	6/24/2009	11/3/2009	19	3.44	21	3.56	40	7.00
2010	6/9/2010	10/5/2010	15	2.45	15	2.75	30	5.20
2011	3/2/2011	12/20/2011	24	3.99	21	3.68	45	7.67
2012	6/7/2012	9/26/2012	12	2.00	12	2.00	24	4.00
2013	9/10/2013	10/10/2013	6	0.67	4	0.67	10	1.33
Total	6/24/2009	10/10/2013	76	12.54	73	12.65	149	25.20

Data collected from Lake Moultrie during the same time period and using the same collection methods was combined with the data collected from Lake Marion to investigate differences in mean TL and condition within species, between lakes, and among years. Differences in mean TL were assessed with a generalized linear mixed model (Proc Glimmix). For data collected between 2009 and 2012 we modeled total length (mm) in relation to year and Lake (fixed effects), site (random effect), and used the covariate day-of-year (DOY) to account for fish growth throughout each sample season. For striped bass a reduced model, restricted to Lake Marion Data, was used to evaluate growth among years in Lake Marion between 2008 and 2012. The 2013 sample data was not included in any modeling due to only collecting fish on two occasions at the end of summer.

To evaluate condition of key species we developed standard weight (W_s) equations by pooling all TL and Wt data within species collected between 2009 and 2012 and regressing LogTL by LogWt. Regression coefficients from species-specific linear regressions were used to calculate $W_s = 10^{a+b \cdot \text{LogTL}}$. Relative weight (W_r) was then calculated for each fish,

$$W_r = \frac{W}{W_s},$$

where W is the weight of an individual fish and W_s is the length-specific standard weight. Analysis of covariance was used to evaluate differences in mean W_r within species, among years, by lake, and the covariates TL and DOY were used to assess the influence of TL and DOY on W_r .

Analysis of variance was used to determine if catch per unit effort (CPUE) for striped bass, white perch and American shad differed between sites and among years for fish captured from Lake Marion during 2009 – 2012. All statistical analyses of growth, condition, and CPUE were performed in SAS. Level of significance was 0.05. Least square means are reported to account for the influence of linear covariates (e.g., TL and DOY).

Diet

Up to 15 of each key species per site were preserved in 10% formalin on every electrofishing sample date during 2009. During 2013 thirty-six (36) American shad collected from Lake Marion between 7 August and 25 November, and 23 American shad collected from Lake Moultrie between 21 August and 12 December were retained for diet analysis. During 2013 American shad were collected with gill nets from pelagic areas to compare with fish captured from shoreline samples during 2009. Between 2010 and 2014 the stomach contents of preserved striped bass, American

shad, and white perch specimens were examined under a dissecting microscope and identified to the lowest practical taxon.

We updated our diet database to include dry weight of prey items so that diet composition by weight could be assessed. Weights for prey item were assigned, calculated, or directly measured. For larval insects, micro crustaceans, and tessellated darters (the most frequently encountered fish in stomach samples) we calculated weight using published length-weight relationships. A sample of adult insects (Midges and Mayflies) was collected from Lake Marion during summer 2013 and processed for dry weights. Those weights were then assigned to appropriate prey items in our data base. Tissue from unidentifiable fish was removed from diet samples, dried at 60°C for 48 h, and weighed.

Results/Discussion

Growth

There were significant differences in total length of YOY striped bass between lakes ($P=0.0048$), among years ($P = 0.0006$), and the covariate DOY was also significant ($P < 0.0001$). The interaction between DOY and year was not significant ($P > 0.05$). Striped bass in Lake Marion (mean TL = 106.7, [95% CL 104.4 – 109.1]) were significantly larger than those caught from Lake Moultrie (mean TL = 87.3, [95% CL 79.4 – 95.1]). Striped bass collected summer 2012 (mean TL = 103.8, SE = 1.6) were significantly larger than those collected during 2009 – 2011 (Figure 1). The absence of an interaction between DOY and year indicates that growth rate during the study period was similar each year (Figure 2). Therefore, fish size during each summer could be related to earlier or later hatching dates or perhaps, different growth rates before our sampling period.

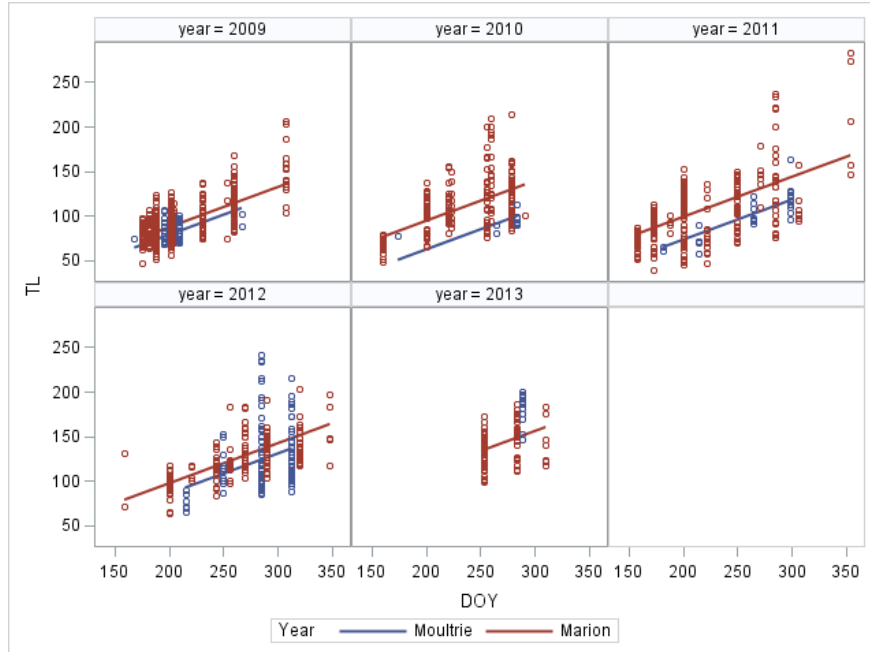
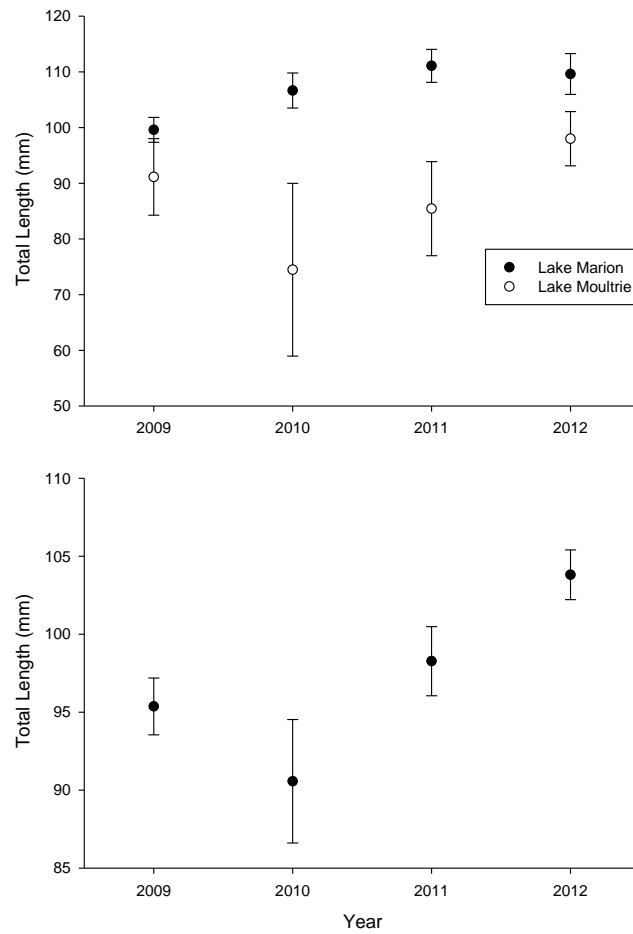


Figure 1. Mean TL of YOY striped bass collected from Lake Marion and Lake Moultrie during summer 2009 – 2012 (Top Panel), and Mean TL of Lake Marion and Lake Moultrie combined (Bottom Panel).

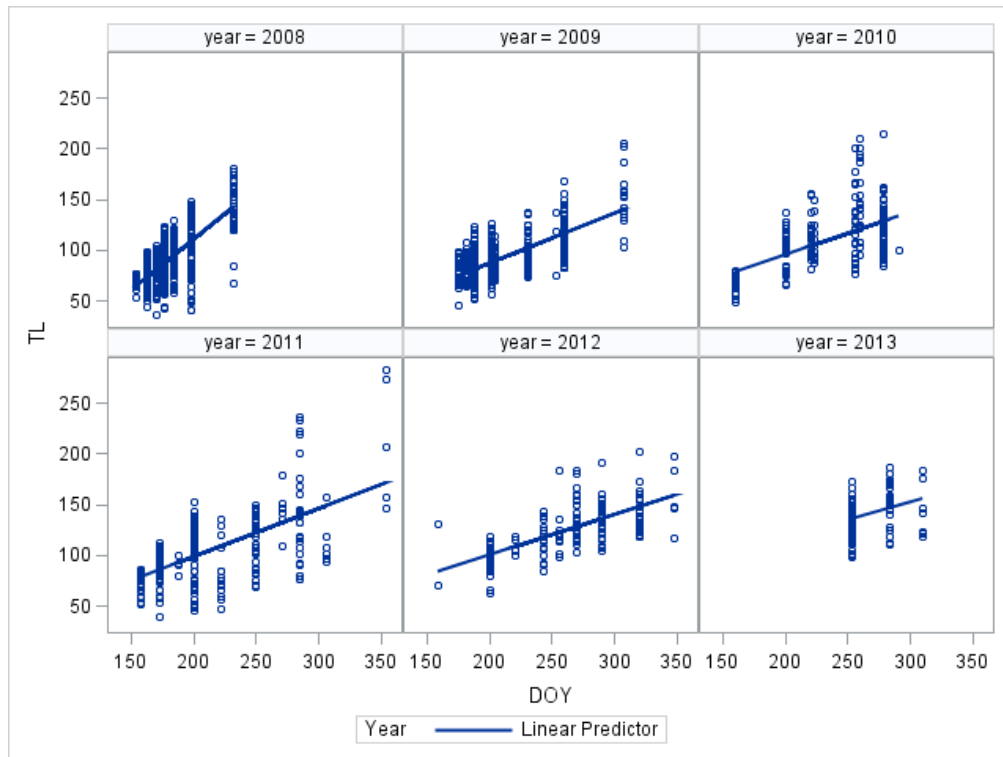


Figure 2. Total length of striped bass YOY by day-of-year for striped bass collected from lakes Marion and Moultrie during 2009 – 2013 (top panel) and total length of striped bass YOY by day-of-year for striped bass collected from Lake Marion 2008 – 2013.

For the reduced model, that only included Lake Marion and also included the 2008 collection; year ($P = <0.001$), the covariate DOY ($P < 0.001$), and the interaction between DOY and year ($P = <0.001$) were significant. Striped bass YOY in Lake Marion were significantly larger during 2008 (mean TL = 117.3, SE = 1.47) than any other year and significantly smaller during 2009 (mean TL = 90.1, SE = 0.96) than any other year (Figure 3). The significant interaction between DOY and year indicated growth was different among years in Lake Marion with 2008 having the fastest growth during the study period among years (Figure 2).

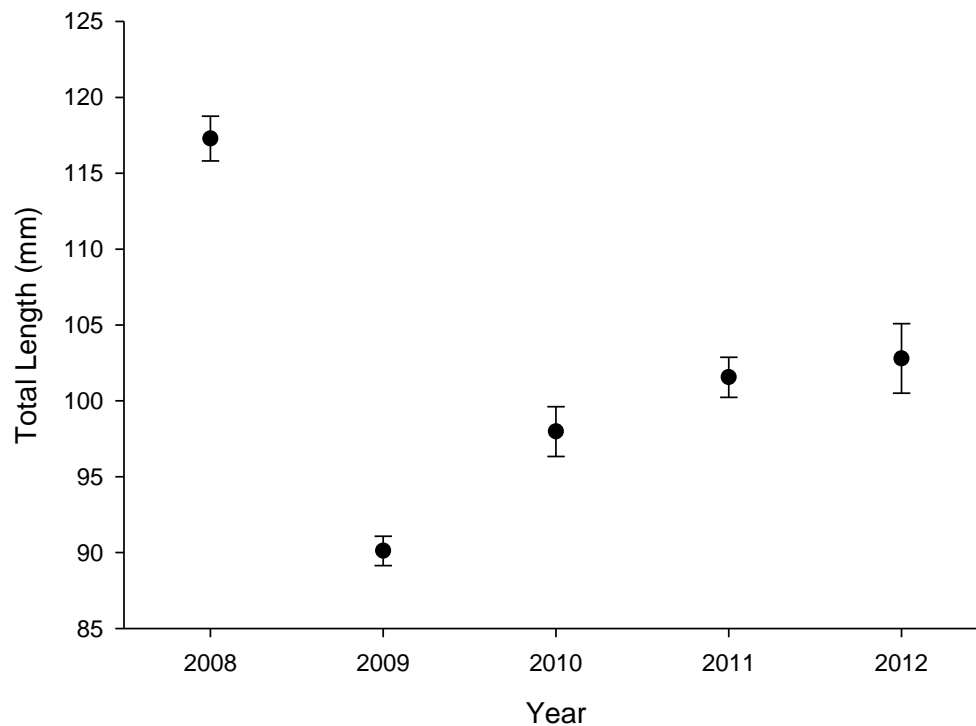


Figure 3. Mean TL and associated 95% confidence intervals for YOY striped bass collected from Lake Marion, SC with shoreline boat electrofishing 2008 – 2012.

For American shad there were significant differences in mean TL among years, the covariate DOY was significant, and the interaction between DOY and year was significant. All other model terms and interactions were insignificant. Mean TL of American shad was greater during 2009 and 2012 than 2010 and 2011 (Table 2). For white perch there were significant differences in mean TL among years, the covariate DOY was significant, and the interactions between DOY and year and DOY and Lake were significant. All other model terms and interactions were insignificant. Mean TL of white perch decreased each year during 2009 to 2011; however, only 2009 and 2011 were significantly different (Table 2).

Table 2. Mean TL of American shad and white perch (upper and lower 95% confidence limits) for fish collected from Lake Marion and Moultrie with shoreline electrofishing during 2009 - 2012. Means with the same letters were not significantly different.

Year	American Shad			White Perch		
	Mean TL	LCL	UCL	Mean TL	LCL	UCL
2009	84.22 ^a	79.61	88.82	69.04 ^a	66.84	71.24
2010	73.24 ^b	68.69	77.78	65.38 ^{ab}	63.18	67.58
2011	75.30 ^b	70.76	79.84	63.97 ^b	61.78	66.16
2012	93.97 ^a	89.32	98.62			

Condition (Wr)

More than 1,200 fish from each species were used to investigate the relationship between length and weight of YOY. There were significant linear relationships between log₁₀TL and log₁₀wt for each species (Table 3). The slope and the intercept from each regression were used to calculate length-specific standard weights (Ws).

Table 3. Length-weight regression coefficients, standard errors in parentheses, for striped bass (STB), American shad (AMS), and white perch (WTP) collected from Lake Marion and Moultrie with shoreline electrofishing during 2009 - 2012.

Species	n	Mean		Wt (g)	Slope (b)	Intercept (a)	r ²
		TL (mm)	TL (mm)				
STB	1,263	103	39 - 222	0.7 - 129.1	2.964 (0.008)	4.884 (0.018)	0.99
AMS	2,590	75	30 - 164	0.3 - 41.7	2.802 (0.001)	4.661 (0.014)	0.98
WTP	3,130	68	35 - 117	0.6 - 22.12	2.894 (0.007)	4.700 (0.014)	0.98

For striped bass there were significant differences in W_r between lakes ($P < 0.0001$), among years ($P < 0.0001$), the covariate DOY ($P < 0.0001$) and the interaction between DOY and year ($P = 0.0035$) were also significant. TL was not a significant predictor of W_r . W_r was significantly higher in Lake Marion (1.01) than Lake Moultrie (0.93). In Lake Marion W_r varied among years and was highest (1.05) in 2010 and lowest (0.96) during 2012, in lake Moultrie W_r was highly variable within years, and lower than that observed in Lake Marion (Figure 4). The interaction between DOY and year indicated there was a slightly negative relationship between W_r and DOY in Lake Moultrie during all years; however, in Lake Marion there was a positive relationship between DOY and W_r in 2009 and 2012 and negative relationship in 2010 and 2011.

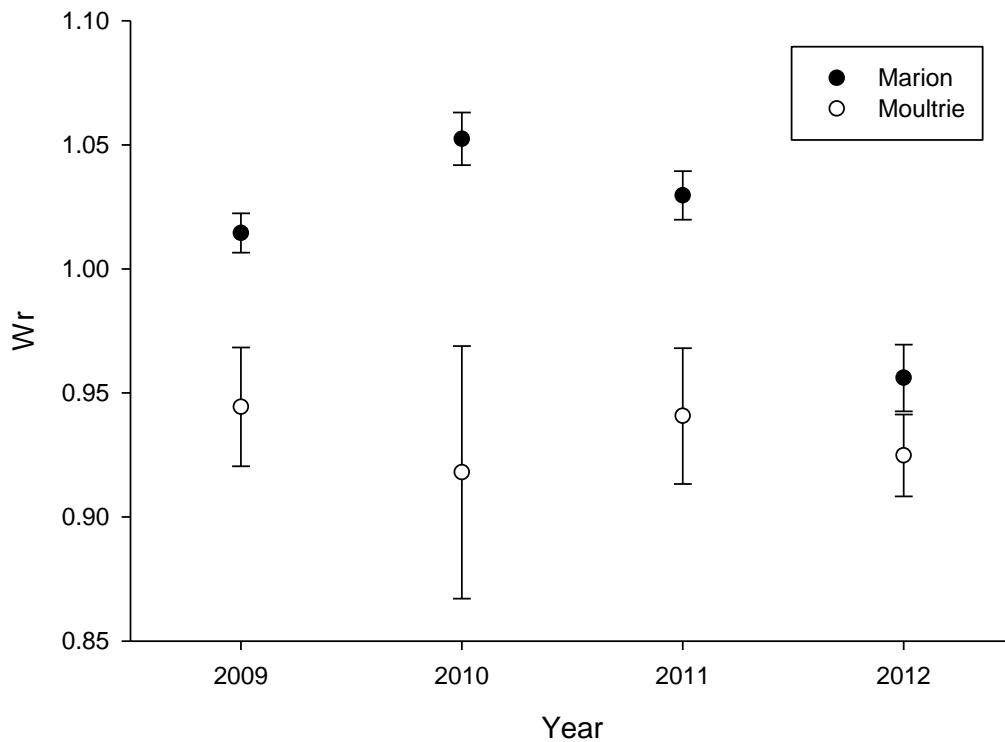


Figure 4. Mean W_r , and associated 95% confidence limits, of YOY striped bass collected from Lake Marion and Lake Moultrie, SC with shoreline boat electrofishing 2009 – 2012.

For American shad there were significant differences in W_r among years ($P < 0.0001$), the covariate DOY ($P < 0.0001$) and the interaction between DOY and Year ($P < 0.0001$) were also significant. There was no difference in W_r between lakes nor was TL a significant predictor of W_r . Mean W_r was 1.01 in Lake Moultrie and 1.00 in Lake Marion. W_r varied among years with the highest W_r observed during 2009 and 2012 (Figure 5). The interaction between DOY and year indicated there was a negative relationship between W_r and DOY in most years, but a slightly positive relationship during 2010.

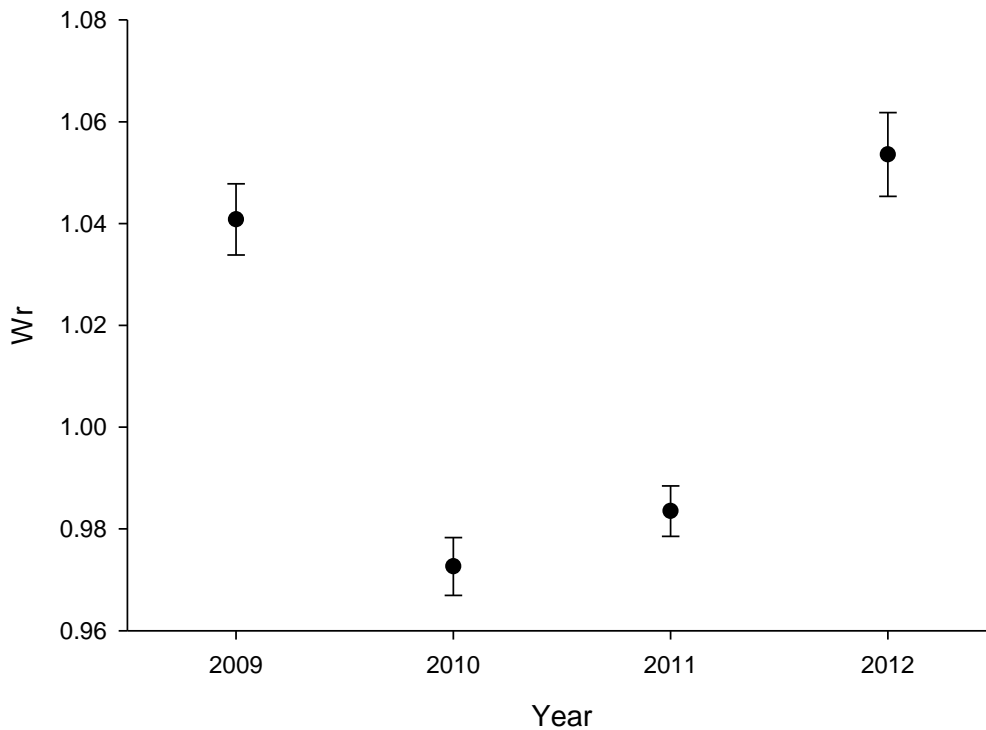


Figure 5. Mean W_r , and associated 95% confidence limits, for YOY American shad collected from Lake Marion and Lake Moultrie, SC with shoreline boat electrofishing 2009 – 2012.

For white perch there were significant differences in W_r among years and between lakes. The covariate DOY and the interaction between DOY and year was also significant. TL was not a significant predictor of W_r . Mean W_r was higher in Lake Marion ($W_r = 1.02$) than Lake Moultrie ($W_r = 0.95$). The highest W_r were observed during 2009 and 2012 in lake Marion and in Lake Moultrie the highest W_r was observed during 2012 (Figure 6). The interaction between DOY and year indicated there was no relationship between W_r and DOY in most years; however, during 2011 there was a negative relationship between DOY and W_r in both Lakes.

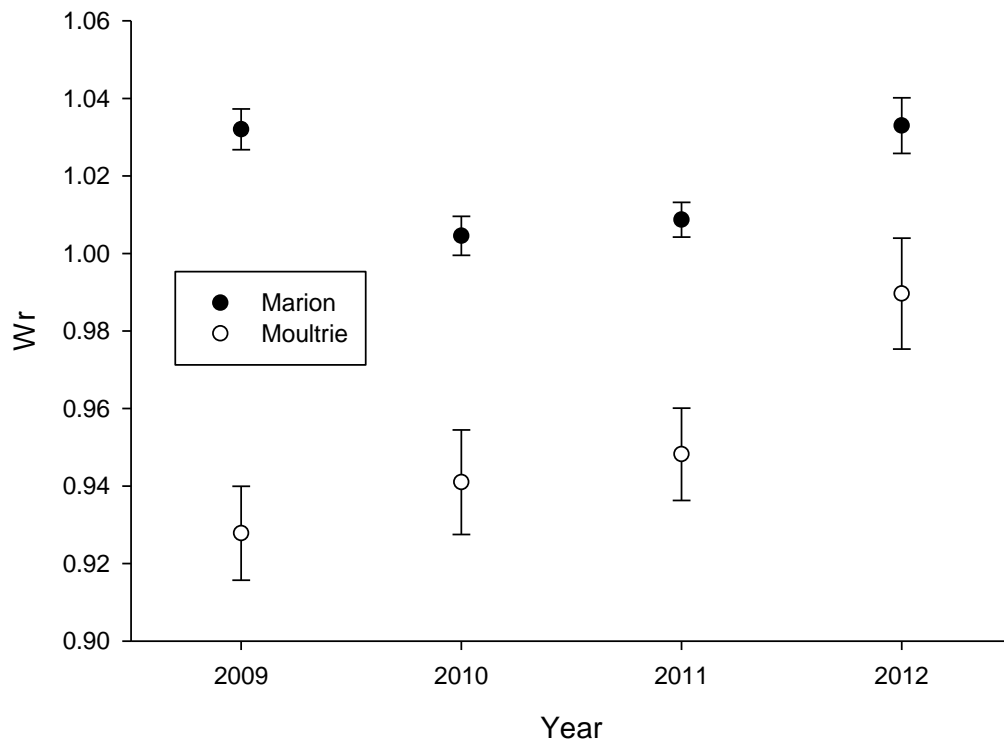


Figure 6. Mean W_r , and associated 95% confidence limits, of YOY white perch collected from Lake Marion and Lake Moultrie, SC with shoreline boat electrofishing 2009 – 2012.

Abundance

CPUE of striped bass did not vary among the two Lake Marion sites, but there were significant differences among years. During 2009 catch rates (99/hour) were much higher than during 2010 – 2012 (Table 4). Our lowest striped bass catch rate (24/hour) was observed during 2012, although not significantly different than 2010 or 2011. CPUE of American shad varied between sites but not among years due to highly variable catch rates within sites. CPUE of American shad was significantly higher at “Big Water” (200/h) than “Indian Bluff” (74/h). CPUE of

white perch varied among years and between sites. CPUE of white perch was significantly higher at “Indian Bluff” (230/h) than “Big Water” (113/h) and was significantly lower during 2012 than 2011.

Table 4. Mean catch per unit effort (n/h) and associated 95% confidence limits for key species collected from Lake Marion and Moultrie with shoreline electrofishing during 2009 - 2012. Mean CPUE with the same letters were not significantly different.

Year	Striped Bass	American Shad	White Perch
2009	99 ^a (72 – 126)	107 (34 – 180)	164 ^{ab} (98 -229)
2010	34 ^b (4 – 64)	208 (128 – 288)	185 ^{ab} (114 – 257)
2011	37 ^b (7 – 67)	183 (103 -263)	265 ^a (193 – 336)
2012	24 ^b (-9 – 57)	52 (-38 – 141)	71 ^b (-9 – 150)

Growth, abundance (CPUE), and Wr of our key species YOY were variable among years and there were site and lake effects for some variables. Growth and Wr of striped bass were higher in Lake Marion than Lake Moultrie. Wr of white perch was higher in Lake Marion than Lake Moultrie. Within Lake Marion catch rates were different between sites for white perch (higher at Indian Bluff) and American shad (higher at Big Water). Preliminary analysis indicates that density-dependent factors within species could be partially responsible for annual variation in growth. For white perch and American shad there was a negative relationship between CPUE and growth. As CPUE increased growth decreased. For striped bass that relationship was less clear, likely due to the consistently low catch rates observed during 2010 - 2012; however, during 2009, the year with the highest catch rates (99 fish/h) striped bass had the slowest growth (Mean TL = 99.6) (Figure 7).

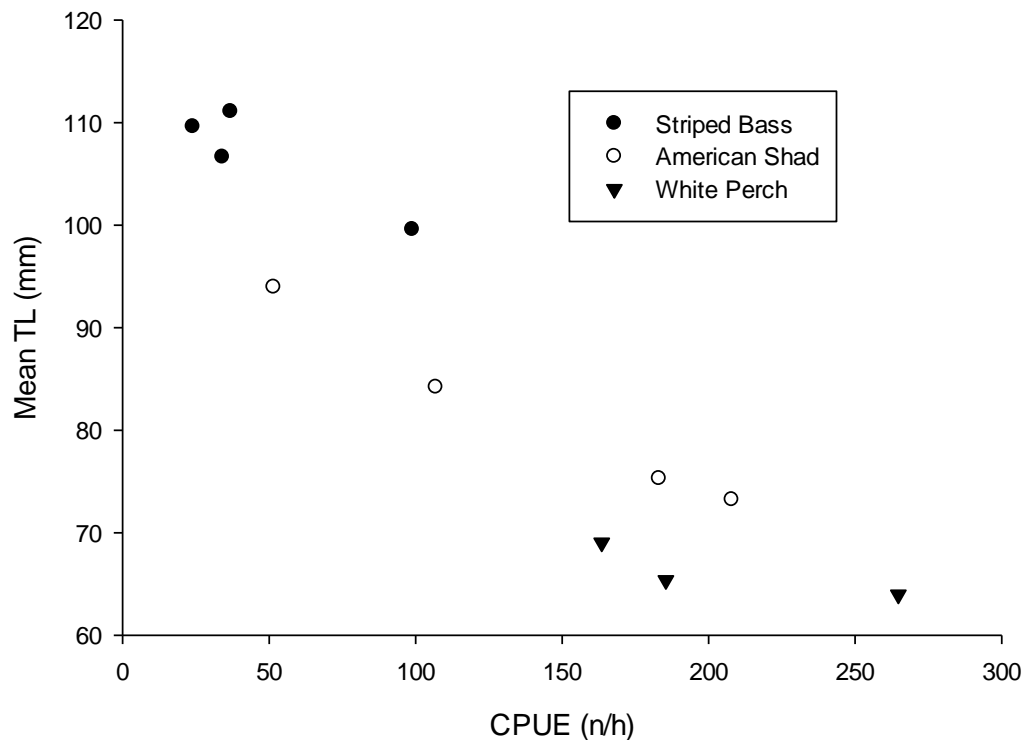


Figure 7. Catch-per-unit-effort (CPUE [n/h]) versus mean total length (TL [mm]) for young-of-year of striped bass, American shad, and white perch collected from Lake Marion, SC with shoreline boat electrofishing 2009 – 2012.

Diet

Weights were generated for 99% of the 24,980 prey items in our diet database which included the stomach contents of 113 striped bass, 120 white perch, and 128 (59 collected during 2013) American shad. During 2009 the Stomach contents of American shad were dominated by insects which accounted for 83% of the prey items encountered (Figure 8). Microcrustaceans (10%) and water mites (Chelicerata) (8%) were the next most abundant, the remaining prey groups accounted for less than 1%. During 2013, from pelagic samples, a much different American shad diet was

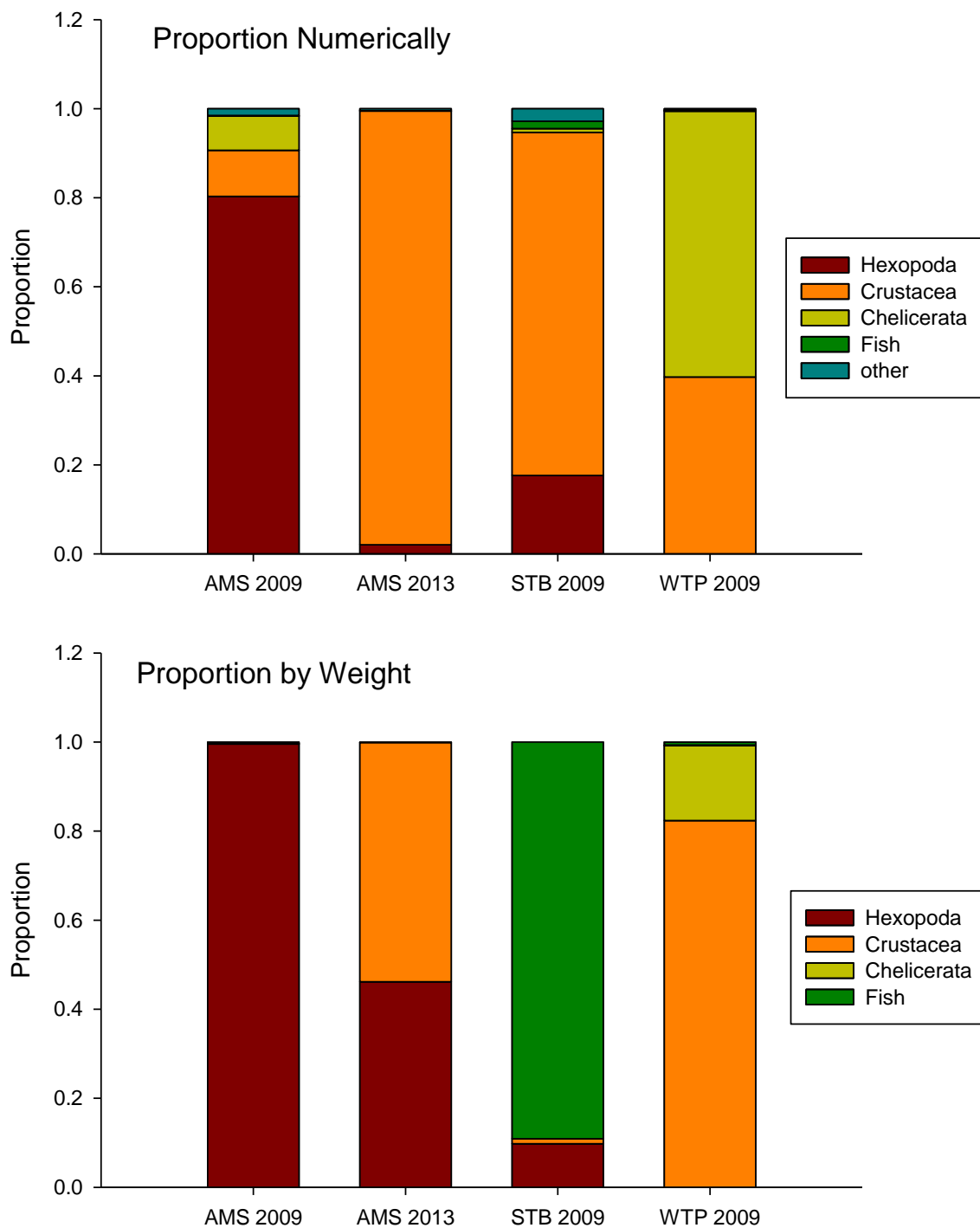


Figure 8. Proportion numerically (top panel) and by weight (bottom panel) of major prey items in the diets of young-of-the-year American shad (AMS), striped bass (STB), and white perch (WTP) collected from littoral areas during 2009 and pelagic areas during 2013 in Lake Marion, South Carolina.

observed where 97% of the items encountered were micro-crustaceans and the remaining prey groups accounted for less than 3% of the diet. The most numerous items encountered in striped bass stomachs were microcrustaceans (77%) and insects (18%) while fish accounted for less than 2%. The most numerous items encountered in white perch were microcrustaceans (59%) and insects (40%).

By weight insects accounted for over 99% of the diet of American shad during 2009; however, during 2013 insects accounted for only 46% of their diet and micro-crustaceans accounted for 54% (Figure 8). Although fish were rare (<2% of total prey items) in the stomach contents of striped bass they accounted for 90% of their diet by weight. Striped bass size influenced diet; for striped bass less than 75 mm TL 50% of their diet by weight was insect, 44% was fish, and 5% was crustacean, for fish greater than 75 mm TL 90% of their diet was fish and only 9% was insect. By weight white perch diets were dominated by insects (81%), but microcrustaceans were also important (18%).

The diet, by weight, of American shad, white perch, and small striped bass (< 75 mm TL) collected from shoreline samples during 2009 consisted largely of insects. However, the potential for competition for insect resources between American shad and the two morone species was diminished because American shad fed primarily on adult insects while the morones (white perch and small striped bass) fed almost exclusively on larval insects (Figure 9). During 2009 and 2013 at least 89% of the insect diet of American shad consisted of adult insects, conversely white perch consumed no adult insects and adult insects contributed only 5% to the diet of small striped bass. During 2013 American shad collected from pelagic areas relied heavily on micro-crustaceans (53% of their diet by wt) resulting in considerable diet overlap among species, assuming white perch inhabit pelagic areas and their diet there is similar to their diet in shoreline habitat.

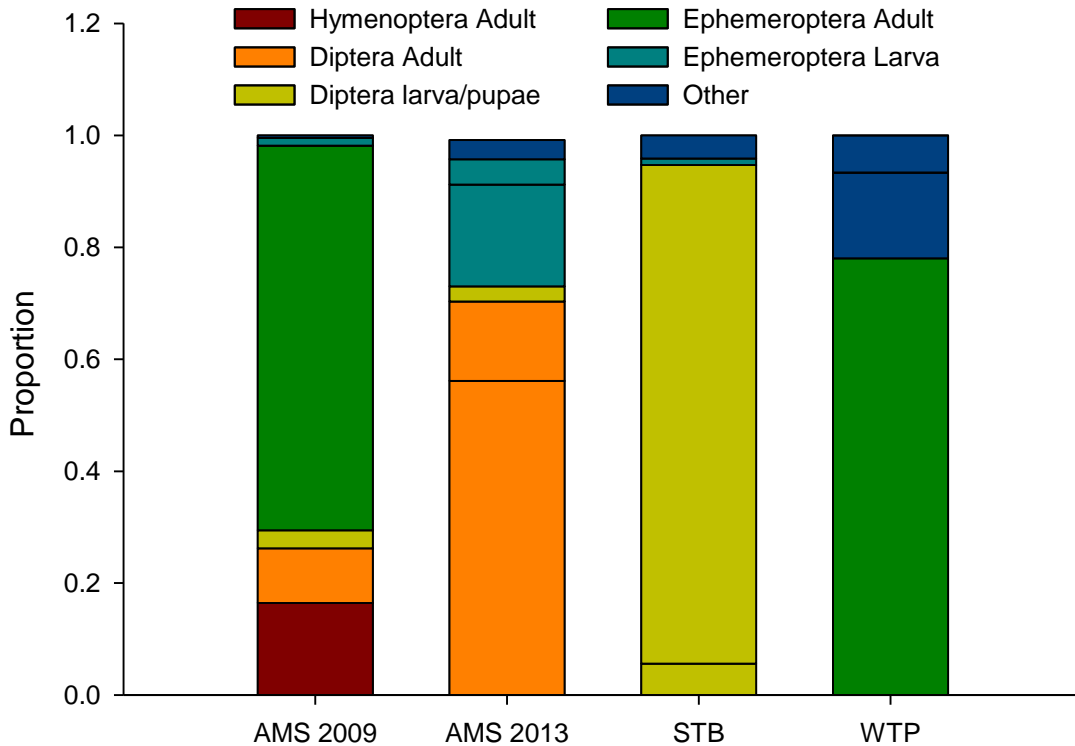


Figure 9. Proportion by weight of insects in the stomachs of American shad (AMS), striped bass (STB) and white perch (WTP) collected from Lake Marion, South Carolina during 2009 and 2013.

American shad appear to be opportunistic surface feeders while small striped bass and white perch are primarily benthic feeders (larval insects) and water column feeders (micro crustaceans). Larger striped bass, those that primarily feed on fish, also routinely consume adult mayflies from the surface. Diet of American shad varied during each summer presumably in relation to the availability of adult insects at the surface. During 2009 most of their energy came from adult insects. Dipteran, Hymenopteran and Emphemeropteran adults were each important prey resource at some point during summer (Figure 10). During late September larval insects were also important. During 2013 when American shad were collected from pelagic areas of Lake Marion and Moultrie, and later in the year, crustaceans were the most important resource on several dates (Figure 10).

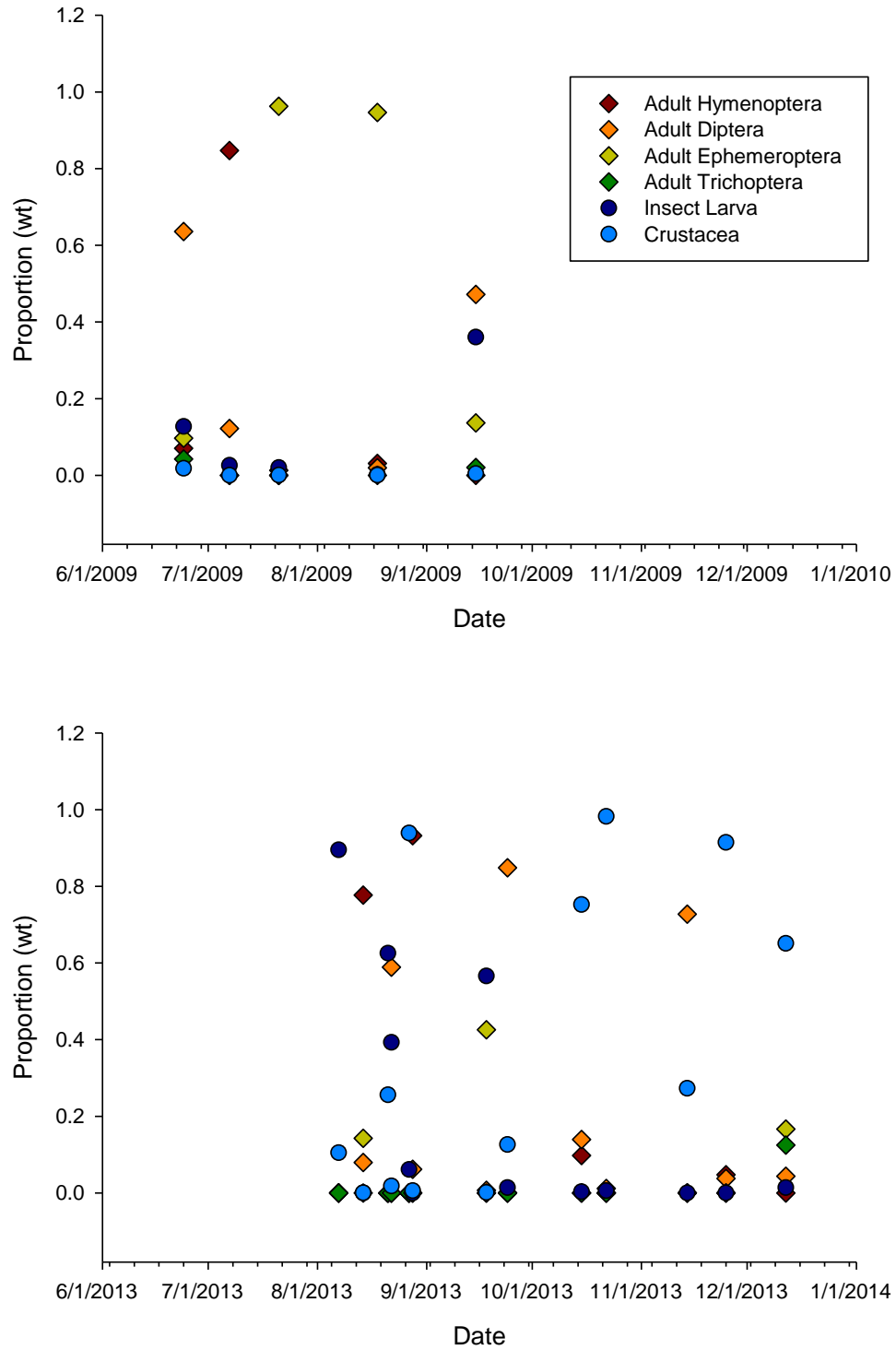


Figure 10. Proportion by weight of prey items in American shad stomachs collected from Lake Marion, South Carolina during 2009 and Lake Marion and Lake Moultrie during 2013.

The 2013 pelagic samples for American shad indicate there is potential for competition among the three species with microcrustaceans being an important component of each. Our study only evaluated diet during summer/fall, during winter and early spring the potential for competition may increase with fewer emerging adult insects.

Recommendations

During 2015 we will complete our analysis of growth, condition and abundance of our key species. A formal diet analysis will be completed to assess the potential for competition among our key species. Genetic samples collected from YOY striped bass during summer 2013 will be processed to examine the contribution of stocked fish at our sample locations.

Job Title: Assessing introgressive hybridization within and habitat requirements of native South Carolina redeye bass

Period Covered July 1, 2013 – June 30, 2014

Summary

Work has continued on the study of redeye bass in South Carolina, the impacts of hybridization among black bass species on redeye populations and associated outreach efforts. Outreach efforts included presentation of past work and completion and final submittal of four manuscripts based on that work. The development of fast genetic assays for use in furthering our understanding of the extent of hybridization in Savannah basin streams has progressed. Assays for two loci, Actin and Calmodulin, have been tested on pure species and hybrids and are working well. We coordinated with Region 1 and with outside partners in the collection of data for the establishment of genetic and habitat baselines in select redeye bass streams. High summer flows in 2013 impacted the ability to collect fish and habitat data, but fish collections for the Chauga and Chatooga Rivers were successfully completed. Work on additional priority streams is ongoing.

Introduction

The redeye bass *Micropterus coosae* (Hubbs and Bailey 1940) is one of two black bass native to South Carolina, and has been identified by South Carolina's Comprehensive Wildlife Conservation Strategy as a Species of Highest Priority due its restricted range and threats from introduced species (Kohlsaet et al. 2005). The species' native range is restricted compared to others of its genus and includes the Savannah, Altamaha and Ogeechee River drainages on the Atlantic slope, and the Mobile Bay and Apalachicola drainages on the Gulf slope. Redeye bass occupy habitats above the Fall Line in fast moving, cool-water streams (Rhode et al. 2009). In addition to

native headwater streams and tributaries, *M. coosae* has thrived within four of the Savannah River basin's man-made reservoirs; Jocassee, Keowee, Hartwell and Russell (Koppelman and Garret 2002).

Recent studies have examined the relationship among populations of redeye bass across the range of the species. Mobile Bay drainage redeye bass are morphologically distinct from Atlantic Slope populations, with the common name Bartram's bass assigned to the latter (Bud Freeman, unpublished data). DNA sequence data supports this distinction, and further suggests species-level divergence between Savannah River redeye bass and those of other Atlantic Slope drainages. Savannah River redeye bass represent a highly divergent and distinct evolutionary lineage (Oswald 2007), and is one of three focus species in the National Fish and Wildlife Foundation's Native Black Bass Initiative (Birdsong et al. 2010).

Introductions of the non-native Alabama bass (*Micropterus henshalli*) into lakes Keowee and Russell have put Savannah River redeye bass at risk due to introgressive hybridization (Barwick et al. 2006). Genetic surveys in 2004 and 2010 showed that Alabama spotted bass have expanded within the drainage, as have their hybrids with redeye bass (Oswald 2007). Both are present in all four lakes surveyed, and in 2010 together they comprised from 48% to 68% of black bass collected from each reservoir. The survey of tributaries of the drainage indicated in 2004 that those redeye populations were for the most part still unimpacted by hybridization, but in 2010 an increase in Alabama bass alleles was noted for several tribs. Alabama bass are known to take advantage of stream habitats, and the continued spread of their alleles throughout the drainage is a possibility.

Current objectives of this study include development of new fast genetic assays, and a longitudinal genetic assessment of redeye bass tributary populations using those assays. Work in the

last year has focused on those objectives, on the presentation of past work, and on multiple publications.

Materials and Methods

Work has continued on development of fast genetic assays. Molecular Beacon software was used to identify suitable probe sequences for three loci, Actin, Calmodulin and ITS. Hydrolysis probes were designed and synthesized for Actin and Calmodulin and have been tested for Alabama Bass, Redeye Bass and hybrids. An alternative approach using species specific PCR primers has been employed for ITS and is still in development. Once fully implemented, these assays together with analysis at the mitochondrial ND2 locus will be used to assess hybridization and to delineate possible refuge areas for redeye bass in seven high priority tributaries.

Fish were collected from priority streams via angling and electrofishing. All black bass collected were weighed (g), measured (tl, mm), photographed, and finclipped. Finclips were stored in 95% ethyl alcohol pending genetic analysis.

Results and Discussion

We have designed sets of hydrolysis probes that target species-specific alleles at the Actin and Calmodulin loci for five species of black bass. The Actin probe was synthesized first and we have tested it against known pure Redeye Bass, Alabama Bass and hybrids. Results are very positive. In a forty cycle run, Redeye Bass and Alabama Bass demonstrate unique patterns, while hybrids demonstrate elements of both (Figure 1).

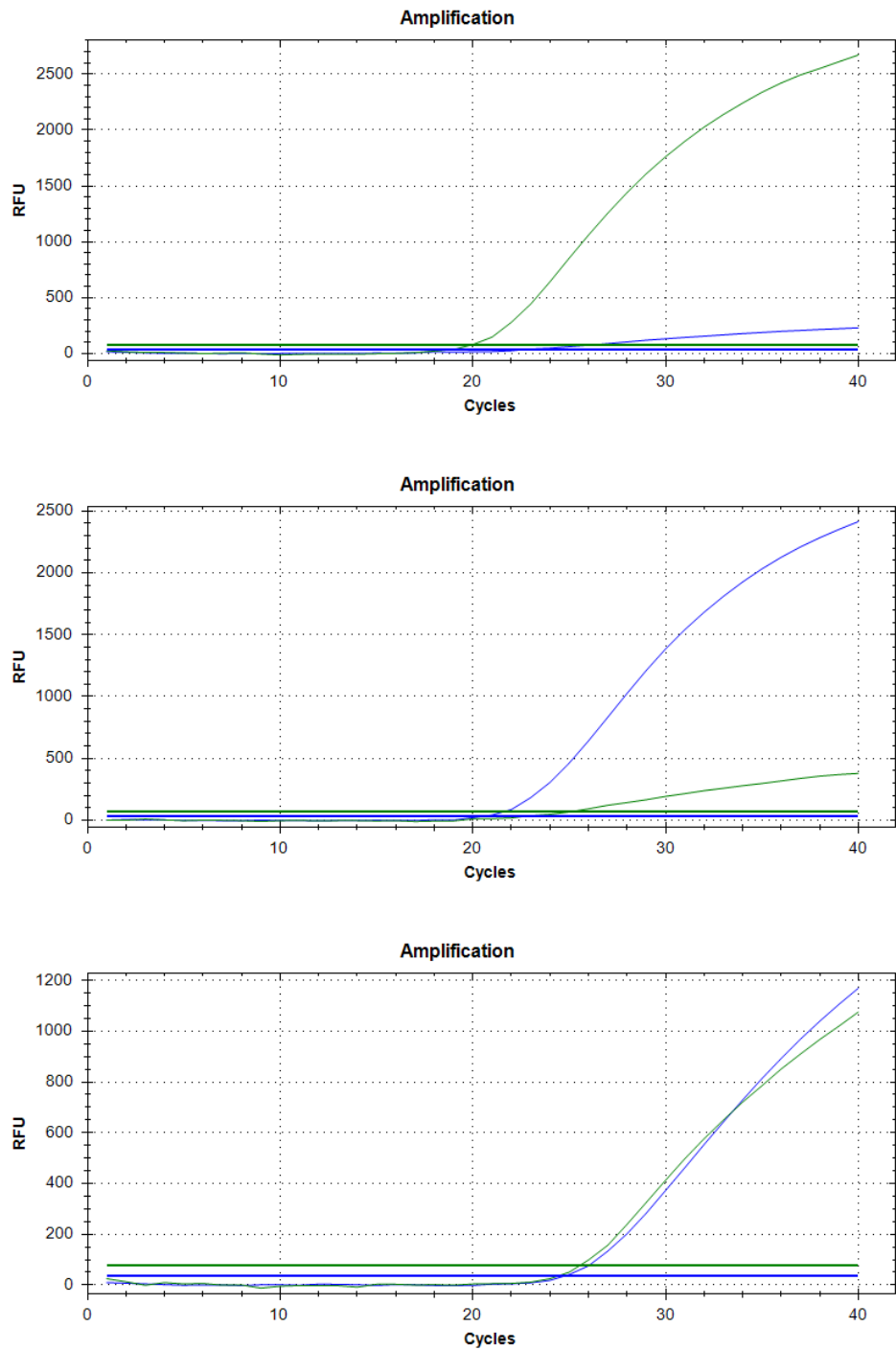


Figure 1. Shown are the results of 40 cycle runs with the Actin hydrolysis probe for Redeye Bass (top), Alabama Bass (middle) and hybrid (bottom) samples.

As was previously reported, Calmodulin probe design was complicated by a pair of closely linked polymorphisms that differentiate Redeye and Alabama Bass near the annealing site for the predicted hydrolysis probe. Molecular Beacon software cannot identify a suitable probe when two site changes are contained within the probe sequence. Instead, we have designed pairs of probes that contain each pair of diagnostic base changes (four possible combinations) within the annealing site. Testing of these probes has also been positive. Pure Redeye Bass, Alabama Bass and hybrids exhibit unique and distinguishable patterns (Figure 2).

Fish and habitat data collections for the longitudinal genetic assessment of tributary populations were complicated by high summer flows. However, fish collections were completed by Region 1 staff on both the Chauga and Chatooga rivers (Table 1). Stream sampling is ongoing, with fish and habitat data collections continuing on priority streams.

In addition to ongoing research and survey work directed at redeye bass conservation, efforts have continued in the presentation and publication of results and in outreach. Past study results were presented at a truncated Black Bass Diversity Symposium held at the Annual Meeting of the American Fisheries Society (AFS) in Little Rock, AK. Three manuscripts based in part on those results, and a redeye bass species profile, all authored or co-authored for publication in the upcoming AFS book 'Black Bass Diversity: Multidisciplinary Science for Conservation', were revised and accepted. Considerable work also went into revisions to an additional manuscript on hybridization in Savannah Basin reservoir populations. We continued to work with a multi-state group focused on black bass conservation in efforts to garner outside funding for needed research on redeye bass in the Savannah Basin, and hosted a group meeting in South Carolina. A grant proposal that would have supported cooperative work on multiple black bass species, and included field studies on redeye bass in the Savannah Basin, was submitted but not awarded funding.

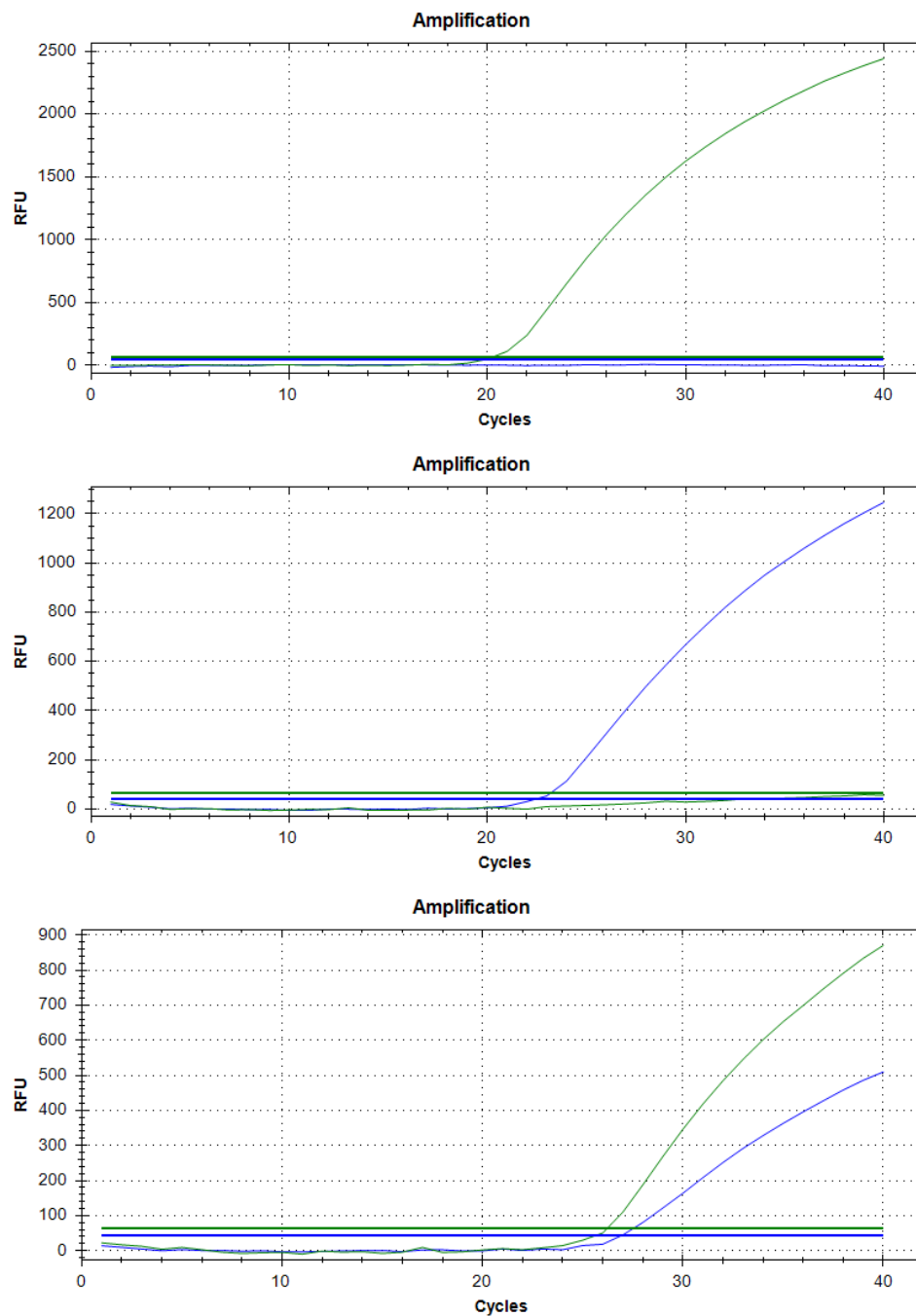


Figure2. Shown are the results of 40 cycle runs with the Calmodulin hydrolysis probe for Redeye Bass (top), Alabama Bass (middle) and hybrid (bottom) samples.

Table 1. Black bass collected from Savannah basin streams in 2013; redeye bass (REB), largemouth bass (LMB), Alabama bass (ALB), redeye x Alabama bass hybrid (RAH).

River	Site	Date Collected	Field ID	N Collected
Chauga River	ChauRam Park	6/26/13	REB	21
	Cobb Bridge	7/24/13	REB	23
	Riley Moore	7/30/13	REB	46
	Lower Jenkins Bridge	8/15/13	REB	9
Chatooga River	Hwy 76	8/1/13	REB	31
	Camp Creek	8/6/13	REB	4
	Opossum Creek	8/27/13	REB	2

In an effort to assist in work to describe Bartram's Bass of the Savannah Basin, we spent time with Bud Freeman from University of Georgia to help him collect redeye bass from Steven's Creek. We consider the description of Bartram's Bass to be a critical step needed in the effort to move conservation of the species forward.

Recommendations

Continue to work with Region 1 and outside partners to examine redeye bass stream populations in the Savannah Basin, to evaluate the extent of hybridization among and within stream populations, to identify refuge areas of pure redeye bass, and to prioritize stream populations and habitats for conservation. Prioritize research and outreach needs associated with Bartram's Bass. Convene a Bartram's Bass Working Group, to include but not be limited to staff from SCDNR and GADNR, to guide continued research and conservation of the species.

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Job Title: Developing Sediment Management Guidelines to Enhance Habitat and Aquatic Resources in the Broad River basin, South Carolina

Period Covered July 1, 2013 – June 30, 2014

Summary

Data collection was conducted for Objective 3 of the Broad River Sediment Management study: Define the relation between aquatic communities and changes in physical habitat (part of a collaborative study with the SCDNR/South Carolina Geological Survey, “Developing Sediment Management Guidelines to Enhance Habitat and Aquatic Resources in the Broad River Basin, South Carolina”). Preliminary relationships among fish assemblage structure, stream habitat and sediment characteristics were explored for potential significance and to guide future analyses. Results thus far suggest aquatic habitats and fish assemblage structure in streams and rivers of the Broad River basin vary in relation to substrate and sediment conditions (i.e. from anthropogenic activities, land use) in addition to natural stream features.

Introduction

Objective 3: Define the relation between aquatic communities and changes in physical habitat.

Sedimentation is a predominant form of aquatic habitat degradation in lotic systems (Waters 1995). Many of the rivers of the South Carolina Piedmont exhibit chronic effects of sedimentation due to historic land use including widespread agriculture. In addition, acute sources such as in-stream sand mining operations may alter sediment dynamics.

The Broad River basin supports a diverse aquatic assemblage including approximately 60 fish species, or more than one third of South Carolina’s native freshwater fish fauna. Many of these species require clean, undisturbed substrates for fulfillment of life history processes including

reproduction. Shoal habitats in particular provide critical spawning grounds for many native fishes such as catostomids, yet these habitats are susceptible to excessive sediment deposition. Effective management of sediment in the Broad River basin is imperative to preserving habitat quality for sustaining these and other native aquatic species.

We aim to characterize relationships among sediment, aquatic habitat condition, and biological assemblages in the Broad River basin. Relationships will be used to develop management targets for maintaining suitable aquatic habitat and species populations in the Broad River basin.

Materials and Methods

Relationships Among Stream Habitat, Sediment and Fish Assemblage Structure

The major tributaries of the Broad River exhibit a wide range of sediment impacts and represent independent units in which downstream habitats are expected to reflect the cumulative influences of land uses and impacts within the watershed (e.g. sedimentation). Ten of 11 study tributaries were sampled in fall 2013 and spring 2014 (Table 1). Sampling was attempted on the Pacolet River but could not be conducted effectively due to persisting high discharge from above-average rainfall in 2013.

Sites were sampled using backpack electrofishing to assess the entire fish assemblage (species composition and relative abundance). Given the large size of most sites, fish sampling was accomplished by using 20 seine sets distributed throughout the sample section in proportion to the amount of area represented by each habitat type (e.g. riffles/shoals, runs, pools). At each set, a 3.05-m (10-ft) seine was set at the downstream end of each habitat unit and an area of approximately 15 m² was sampled immediately upstream of the seine by a single backpack electrofisher, working all fish downstream to the seine. A 6.10-m (20-ft) seine was used on the Broad River main stem to

provide better coverage of the large shoal areas. All fish were identified and enumerated at each set, providing a measure of fish assemblage composition by habitat units as well as by site. In addition, habitat (depth, velocity and macrohabitat type) and substrate samples were obtained at each set in collaboration with SCDNR/South Carolina Geological Survey staff to provide a detailed measure of substrate and sediment characteristics of each site.

Table 1. Sample sites for habitat and fish assemblage monitoring in the Broad River basin and sample status for Fall 2013 and Spring 2014 (X = sample completed).

Fish Assemblage / Habitat Assessment	Latitude	Longitude	Fall 2013	Spring 2014
Kings Creek	35.04313	-81.47615	X	X
Thicketty Creek	34.91475	-81.49633	X	X
Bullock Creek	34.85863	-81.45410	X	X
Turkey Creek	34.77659	-81.43230	X	X
Sandy River	34.59330	-81.39315	X	X
Duncan Creek	34.48915	-81.59143	X	X
Lawsons Fork Creek	34.94247	-81.78876	X	X
Buffalo Creek	35.12387	-81.56114	X	X
Pacolet River	34.87400	-81.53132	*	*
Tyger River	34.53600	-81.54788	X	X
Enoree River	34.50912	-81.59832	X	X
Broad River (upstream of Tyger River confluence)	34.49545	-81.42275	X	X
Broad River (downstream of Tyger River confluence)	34.48219	-81.42209	X	X
Fish Spawning / Habitat Assessment	Latitude	Longitude	Spring 2014	
Kings Creek (reference/forested)	35.04313	-81.47615		X
Lawsons Fork Creek (impacted/urbanized)	34.94247	-81.78876		X
Broad River (upstream of Tyger River confluence; reference)	34.49545	-81.42275		*
Broad River (downstream of Tyger River confluence; impacted)	34.48219	-81.42209		*
Sand Mine Assessment	Latitude	Longitude	Fall 2013	Spring 2014
North Pacolet River (upstream of Slater Mine extraction)	35.18452	-82.08780	X	X
North Pacolet River (downstream of Slater Mine extraction)	35.18471	-82.08370	X	X

*Sampling could not be conducted due to persistent high flows.

A preliminary assessment of potential relationships among habitat, sediment and fish assemblage structure was conducted. Habitat, substrate and sediment data are currently being processed. To characterize potential influences of sediment on aquatic habitats and fish assemblages, available data on a range of substrate and sediment measures were obtained from the hydrogeological monitoring sites (K. Castle, SCDNR/South Carolina Geological Survey; Table 2), which are located at the fish sampling sites. Since aquatic habitats and biota may respond to both chronic and acute impacts of sedimentation, several measures of suspended sediment yield (LOADEST, SedYield and SPARROW) and deposited sediment composition (PctFine, D50) were explored. These data are preliminary and may vary slightly in time span among sites; they are used here solely to investigate potential relationships and guide future analyses. Most of the data were measured between spring/summer 2012 and summer 2013 and thus provide a reasonable representation of overarching habitat and sediment conditions among sites.

Non-metric multidimensional scaling (NMS) ordination was performed using PC-ORD (Version 5) on the fish assemblage data (abundance) from the 17 samples conducted in spring and fall 2013 to evaluate potential patterns in fish assemblage structure among samples (primary matrix). To explore relationships among fish assemblage structure and environmental, habitat and sediment characteristics, these additional measures were included as a secondary matrix in the ordination (Table 2). Various transformations of the data were performed and the variation in fish assemblage structure among samples was examined in relation to correlations with the environmental, habitat and sediment variables.

Table 2. Environmental, habitat and sediment variables used in NMS ordination to investigate relationships among fish assemblage structure, habitat and sediment characteristics in tributaries of the Broad River. Values reflect data collected from 2012-2013.

Variable	Units	Definition	Mean	Range
Elev	feet	Site elevation	410.6	316 – 551
LOADEST	tons/km ² /yr	Modeled annual suspended sediment yield, standardized to watershed area	89.4	1.5 – 282.8
SedYield	tons/km ² /yr	Observed annual suspended sediment yield, standardized to watershed area	90.1	2.5 – 235.6
SPARROW	tons/km ² /yr	USGS SPARROW model annual suspended sediment yield, standardized to watershed area	157.6	103.1 – 305.8
D50	mm	Mean of all bed sample median particle diameters	1.2	0.7 – 3.3
PctFine	Percentage	Mean percentage by dry weight of fine sediment (sand \leq 2 mm diameter and mud) in bed samples	78.1	42.2 – 93.0
Width	m	Mean wetted stream width	14.9	6.5 – 39.0
Depth	m	Mean water depth	0.5	0.3 – 0.6
DepthSD	m	Standard deviation of water depth	0.2	0.1 – 0.3
Veloc	m/sec	Mean current velocity, measured at 60% water depth	0.3	0.1 – 0.5
VelocSD	m/sec	Standard deviation of current velocity	0.2	0.1 – 0.3
Cond	μ S/cm	Conductivity	100.1	67 – 168

Evaluation of Fish Spawning Habitat Use in Relation to Substrate and Sediment Composition

Sites possessing shoal habitats of contrasting expected sediment impacts were sampled at regular intervals during the fish spawning season on two tributaries of the Broad River, Kings Creek (forested watershed; low sediment impact) and Lawson's Fork Creek (urbanized watershed; high

sediment impact). Aside from land use and sediment load, these streams are similar in drainage area (Kings = 175 km²; Lawsons Fork = 216 km²), channel size, elevation (Kings = 517 ft; Lawsons Fork = 551 ft) and support many of the same shoal/riffle-spawning fish species. However, Lawsons Fork Creek exhibits a disproportionately high observed and modeled sediment yield relative to its drainage area (193.5 tons/km²/yr observed) whereas Kings Creek is considerably lower (3.3 tons/km²/yr observed; K. Castle, SCDNR/South Carolina Geological Survey, pers. comm.).

With one exception, Kings Creek and Lawson's Fork Creek were both sampled on 11 March, 24 March, 31 March, 11 April, 18 April, 01 May, 07 May, 22 May and 03 June 2014 for a total of nine concurrent samples. Lawson's Fork Creek was not sampled on 11 March 2014 due to high discharge. Mean water temperature for Kings Creek during this period was 15.9 C (range 5.9 – 24.4 C) and mean temperature for Lawson's Fork Creek was 16.5 C (range 7.6 – 24.3 C). The Broad River upstream and downstream of the Tyger River confluence could not be regularly sampled for fish eggs in spring 2014 due to high flows persisting from the above-average rainfall in the preceding year. Based on previous attempts, it was determined that egg sampling could not be conducted effectively on the Broad River when discharge was greater than 2,500 cfs at the Carlisle flow gauge.

Shoals were sampled using a 0.09 m² (1 ft²) Surber sampler (Wildlife Supply Company, Inc., Yulee, FL, USA) at 10 – 20 sets (depending on shoal size) across one to two transects spanning each study shoal. The Surber sampler bag mesh and collection cylinder screen mesh size were 500 µm. At each set, the substrate within the sampler area was disturbed by hand for 20 seconds and to a substrate depth of no greater than 5 cm or the maximum possible depth if less than 5 cm. All material collected in the bag and cylinder was preserved in 5% formalin for laboratory examination for fish eggs, larvae and macroinvertebrates. Important habitat features including depth, current

velocity, substrate composition and particle size distribution were measured at each collection point to facilitate an assessment of spawning in relation to habitat condition.

Influence of Sand Mining on Local Habitat, Sediment and Fish Assemblage Structure

The potential local impacts of sand mining on stream habitat and fish assemblage composition were examined at two sites bracketing an active sand mining operation on the North Pacolet River in the Broad River basin. The sand mining operation consisted of an approximately 250-m-long sand extraction zone within which a barge is used to vacuum substrate, which is then sorted to extract sand of various sizes. Extracted water was continuously returned to the river at the downstream end of the extraction zone. To assess potential local influences of this operation on adjacent habitats and fish assemblages, one sample site was selected immediately upstream of the extraction zone and another site was selected immediately downstream of the extraction reach. Sites were sampled using backpack electrofishing to assess the entire fish assemblage (species composition and relative abundance) in identical fashion to the tributaries as explained previously. In addition, habitat (depth, velocity and macrohabitat type) and substrate samples were obtained at each fish collection location in collaboration with SCDNR/South Carolina Geological Survey staff to provide a detailed measure of substrate and sediment characteristics of each site.

Results

Relationships Among Stream Habitat, Sediment and Fish Assemblage Structure

Thirty-five (35) species of fish were collected altogether among the Broad River tributary monitoring sites in fall 2013 (Table 3). Fish species richness among tributary samples in fall 2013 averaged 14.7 and ranged from 6 (Tyger River) to 20 (Sandy River). The most abundant species overall in fall 2013 were *Hybognathus regius* (Eastern Silvery Minnow), *Cyprinella nivea* (Whitefin

Table 3. Fish species collected at 10 tributary monitoring sites in the Broad River basin, fall 2013. Sites are listed in Table 1 in Methods.

Code	Species	Common Name	Number of Sites Present	Total Catch	Relative Abundance
NHS	<i>Hypentelium nigricans</i>	Northern Hog Sucker	5	22	0.88%
NLR	<i>Moxostoma collapsum</i>	Notchlip Redhorse	1	1	0.04%
STJ	<i>Scartomyzon rupiscartes</i>	Striped Jumprock	3	12	0.48%
BJR	<i>Scartomyzon sp.</i>	Brassy Jumprock	2	4	0.16%
FLR	<i>Centrarchus macropterus</i>	Flier	1	1	0.04%
RBS	<i>Lepomis auritus</i>	Redbreast Sunfish	10	93	3.73%
GSF	<i>Lepomis cyanellus</i>	Green Sunfish	4	12	0.48%
PPS	<i>Lepomis gibbosus</i>	Pumpkinseed	1	2	0.08%
BLG	<i>Lepomis macrochirus</i>	Bluegill	6	27	1.08%
RES	<i>Lepomis microlophus</i>	Redear Sunfish	1	2	0.08%
SMB	<i>Micropterus dolomieu</i>	Smallmouth Bass	1	2	0.08%
LMB	<i>Micropterus salmoides</i>	Largemouth Bass	4	6	0.24%
GFS	<i>Cyprinella chloristia</i>	Greenfin Shiner	9	239	9.59%
TLC	<i>Cyprinella labrosa</i>	Thicklip Chub	2	3	0.12%
WFS	<i>Cyprinella nivea</i>	Whitefin Shiner	10	329	13.20%
STC	<i>Cyprinella zanema</i>	Santee Chub	6	60	2.41%
ESM	<i>Hybognathus regius</i>	Eastern Silvery Minnow	6	770	30.89%
HBC	<i>Hybopsis hypsinotus</i>	Highback Chub	1	1	0.04%
BHC	<i>Nocomis leptcephalus</i>	Bluehead Chub	8	230	9.23%
GHS	<i>Notropis chlorocephalus</i>	Greenhead Shiner	6	14	0.56%
STS	<i>Notropis hudsonius</i>	Spottail Shiner	7	132	5.29%
SWS	<i>Notropis procne</i>	Swallowtail Shiner	5	71	2.85%
SBS	<i>Notropis scepticus</i>	Sandbar Shiner	9	178	7.14%
SBH	<i>Ameiurus brunneus</i>	Snail Bullhead	3	6	0.24%
WCF	<i>Ameiurus catus</i>	White Catfish	1	3	0.12%
FBH	<i>Ameiurus platycephalus</i>	Flat Bullhead	2	3	0.12%
CCF	<i>Ictalurus punctatus</i>	Channel Catfish	3	6	0.24%
MGM	<i>Noturus insignis</i>	Margined Madtom	5	39	1.56%
FCF	<i>Pylodictis olivaris</i>	Flathead Catfish	1	1	0.04%
FTD	<i>Etheostoma brevispinum</i>	Carolina Fantail Darter	1	9	0.36%
SWD	<i>Etheostoma fusiforme</i>	Swamp Darter	1	1	0.04%
TSD	<i>Etheostoma olmstedii</i>	Tessellated Darter	7	112	4.49%
SGD	<i>Etheostoma thalassinum</i>	Seagreen Darter	5	72	2.89%
PDD	<i>Percina crassa</i>	Piedmont Darter	8	25	1.00%
MSQ	<i>Gambusia holbrooki</i>	Eastern Mosquitofish	2	5	0.20%

Shiner) and *Cyprinella chloristia* (Greenfin Shiner; Table 3). Species occurring in the most samples were *C. nivea* and *Lepomis auritus* (Redbreast Sunfish; all samples), *C. chloristia* and *Notropis scepticus* (Sandbar Shiner; nine samples), and *Nocomis leptocephalus* (Bluehead Chub) and *Percina crassa* (Piedmont Darter; eight samples).

Thirty-seven (37) species of fish were collected altogether among the Broad River tributary monitoring sites in spring 2014 (Table 4). Fish species richness among tributaries in spring 2014 averaged 14.4 and ranged from 7 (Enoree River) to 19 (Sandy River). The most abundant species overall in spring 2014 were *L. auritus*, *C. nivea* and *N. leptocephalus* (Table 4). Species occurring in the most samples were *C. nivea* and *L. auritus* (all samples), *C. chloristia* and *N. scepticus*.

Using 17 samples from spring and fall 2013, NMS ordination showed a pattern in fish assemblage structure among samples that was more pronounced than expected by chance (Monte Carlo test, $P = 0.004$; final stress = 11.80). About 88% of the total variation in fish assemblage structure among samples was represented by two dimensions in NMS, with Axis 2 representing the majority of variation (51%) and Axis 1 representing about 37% (Figure 1).

Correlations among environmental (including habitat and sediment) variables and the primary ordination axes indicated that fish assemblage structure varied in relation to both environmental/site characteristics and habitat/sediment conditions (Table 5). Variables associated most strongly with Axis 2 included mean width, mean depth and the SPARROW-modeled suspended sediment yield (Kendall's tau; Table 5). Variables associated most strongly with Axis 1 were mean velocity, site elevation, d50 (median bed particle size) and percent fine bed material.

Table 4. Fish species collected at 10 tributary monitoring sites in the Broad River basin, spring 2014. Sites are listed in Table 1 in Methods.

Code	Species	Common name	Number of Sites Present	Total Catch	Relative Abundance
WHS	<i>Catostomus commersoni</i>	White Sucker	1	1	0.12%
CCS	<i>Erimyzon oblongus</i>	Creek Chubsucker	1	1	0.12%
NHS	<i>Hypentelium nigricans</i>	Northern Hog Sucker	7	8	0.98%
NLR	<i>Moxostoma collapsum</i>	Notchlip Redhorse	2	3	0.37%
STJ	<i>Scartomyzon rupiscartes</i>	Striped Jumprock	5	8	0.98%
BJR	<i>Scartomyzon sp.</i>	Brassy Jumprock	1	2	0.25%
FLR	<i>Centrarchus macropterus</i>	Flier	1	4	0.49%
RBS	<i>Lepomis auritus</i>	Redbreast Sunfish	10	140	17.16%
GSF	<i>Lepomis cyanellus</i>	Green Sunfish	5	34	4.17%
WAR	<i>Lepomis gulosus</i>	Warmouth	1	1	0.12%
BLG	<i>Lepomis macrochirus</i>	Bluegill	7	12	1.47%
RES	<i>Lepomis microlophus</i>	Redear Sunfish	1	1	0.12%
SMB	<i>Micropterus dolomieu</i>	Smallmouth Bass	2	2	0.25%
LMB	<i>Micropterus salmoides</i>	Largemouth Bass	2	3	0.37%
TFS	<i>Dorosoma petenense</i>	Threadfin Shad	1	23	2.82%
RSD	<i>Clinostomus funduloides</i>	Rosyside Dace	1	1	0.12%
GFS	<i>Cyprinella chloristia</i>	Greenfin Shiner	9	73	8.95%
TLC	<i>Cyprinella labrosa</i>	Thicklip Chub	1	2	0.25%
WFS	<i>Cyprinella nivea</i>	Whitefin Shiner	10	94	11.52%
STC	<i>Cyprinella zanema</i>	Santee Chub	6	23	2.82%
ESM	<i>Hybognathus regius</i>	Eastern Silvery Minnow	4	42	5.15%
BHC	<i>Nocomis leptcephalus</i>	Bluehead Chub	7	88	10.78%
GLS	<i>Notemigonus crysoleucas</i>	Golden Shiner	1	1	0.12%
GHS	<i>Notropis chlorocephalus</i>	Greenhead Shiner	2	5	0.61%
STS	<i>Notropis hudsonius</i>	Spottail Shiner	5	31	3.80%
SWS	<i>Notropis procne</i>	Swallowtail Shiner	2	6	0.74%
SBS	<i>Notropis scepticus</i>	Sandbar Shiner	8	77	9.44%
SBH	<i>Ameiurus brunneus</i>	Snail Bullhead	4	4	0.49%
YBH	<i>Ameiurus natalis</i>	Yellow Bullhead	1	1	0.12%
FBH	<i>Ameiurus platycephalus</i>	Flat Bullhead	6	16	1.96%
CCF	<i>Ictalurus punctatus</i>	Channel Catfish	2	4	0.49%
MGM	<i>Noturus insignis</i>	Margined Madtom	7	18	2.21%
FTD	<i>Etheostoma brevispinum</i>	Carolina Fantail Darter	1	2	0.25%
TSD	<i>Etheostoma olmstedii</i>	Tessellated Darter	7	36	4.41%
SGD	<i>Etheostoma thalassinum</i>	Seagreen Darter	4	19	2.33%
PDD	<i>Percina crassa</i>	Piedmont Darter	7	28	3.43%
MSQ	<i>Gambusia holbrooki</i>	Eastern Mosquitofish	2	2	0.25%

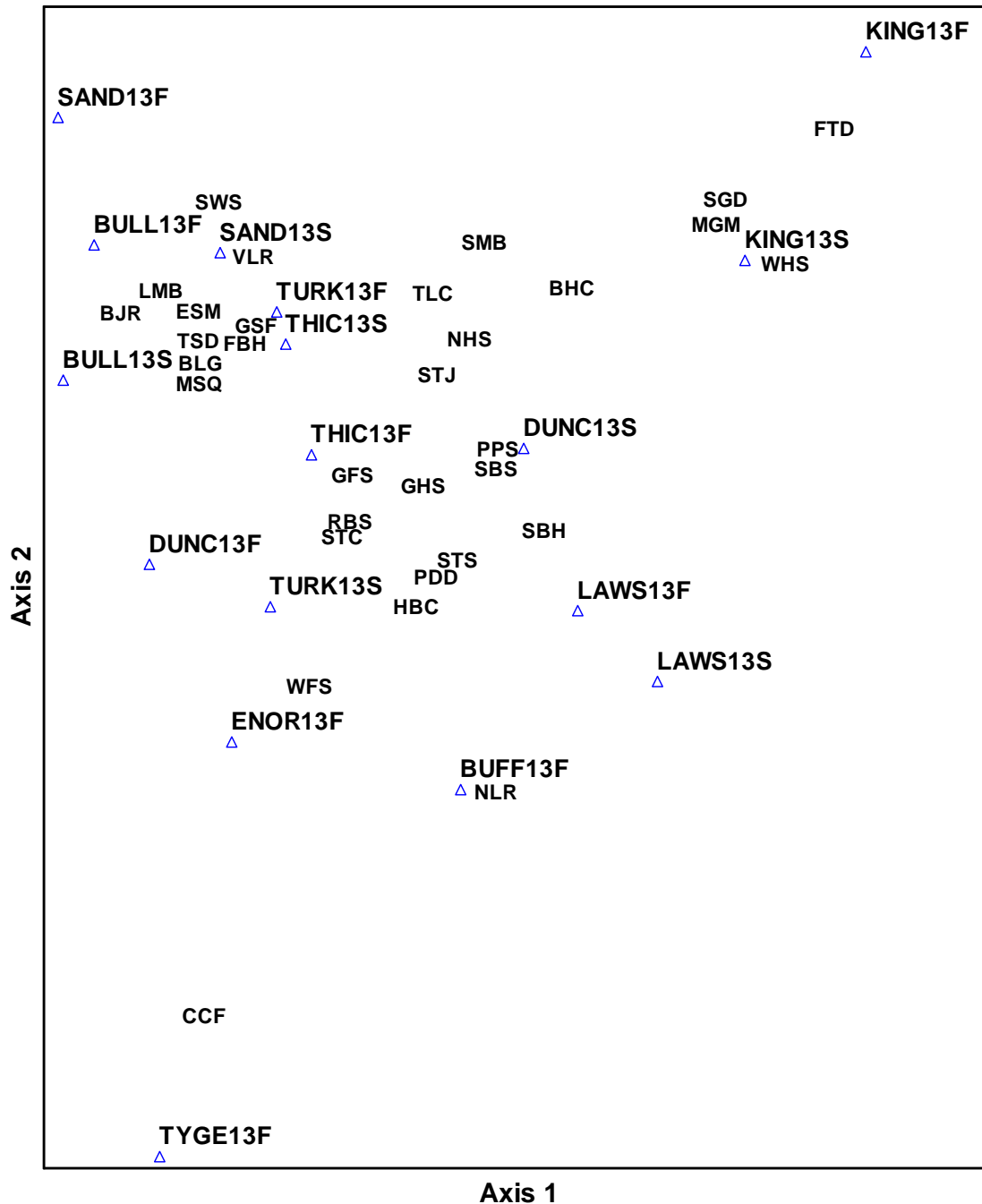


Figure 1. NMS ordination plot of 17 Broad River tributary samples from spring and fall 2013. Sample labels show the first four letters of the site followed by the year (13) and season (S = spring; F = fall). Species are shown as three-letter codes (refer to Tables 3 and 4). Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%.

Table 5. Correlations among environmental, habitat and sediment variables and fish assemblage structure with all 17 tributary samples included (spring and fall 2013). Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%. Variables are defined in Table 2.

	AXIS 1		AXIS 2	
	r	tau	r	tau
Elev	0.719	0.434	0.016	0.008
LOADEST	-0.197	-0.023	-0.190	-0.189
SedYield	-0.054	0.038	-0.453	-0.249
SPARROW	0.287	0.264	-0.516	-0.506
D50mm	0.723	0.385	0.443	0.219
PctFine	-0.666	-0.385	-0.457	-0.249
Width	-0.190	0.015	-0.772	-0.515
Depth	-0.045	0.075	-0.738	-0.508
DepthSD	-0.063	-0.008	0.412	0.219
Veloc	0.596	0.444	-0.461	-0.385
VelocSD	0.485	0.367	0.040	-0.112
Cond	-0.108	0.000	0.593	0.400

Based on the initial ordination, general site characteristics including mean width and depth were playing a large role in the variation in fish assemblage structure among samples. Examination of these variables showed an apparent disproportionate influence of two much larger sites, Enoree River (mean width = 31.4 m) and Tyger River (39.0 m), on the ordination. The mean width of all other sample sites was 12.2 m and none exceeded 18.4 m. To reduce the influence of these two significantly larger sites on the ordination, a second run was performed excluding the Enoree River and Tyger River.

With 15 samples (Enoree and Tyger excluded), NMS ordination in three dimensions represented about 95% of the total variation in fish assemblage structure among samples (Monte

Carlo test, $P = 0.004$; final stress = 6.36). Axis 1 represented the majority of the variation (56%), with Axes 2 and 3 representing about 18% and 21%, respectively.

Correlations among environmental (including habitat and sediment) variables and the primary ordination axes again suggested that fish assemblage structure varied in relation to both environmental/site characteristics and habitat/sediment conditions (Table 6). Variables associated most strongly with Axis 1 (Kendall's tau) included mean velocity, d50 (median bed particle size) and percent fine bed material (Table 6). Variables most strongly associated with Axis 3 were SPARROW-modeled suspended sediment yield, elevation, LOADEST-modeled sediment yield and observed suspended sediment yield.

Table 6. Correlations among environmental, habitat and sediment variables and fish assemblage structure for 15 tributary samples (spring and fall 2013, excluding Enoree and Tyger). Axis 1 represented the majority of variation in fish assemblage structure (56%), Axis 3 about 21% and Axis 2 about 18%. Variables are defined in Table 2.

	AXIS 1		AXIS 2		AXIS 3	
	r	tau	r	tau	r	tau
Elev	0.659	0.353	0.585	0.373	0.401	0.255
LOADEST	-0.136	-0.157	-0.128	0.177	-0.347	-0.177
SedYield	0.070	-0.078	0.217	0.255	-0.266	-0.177
SPARROW	0.411	0.314	0.531	0.255	-0.360	-0.490
D50mm	0.639	0.471	-0.409	-0.137	0.599	-0.020
PctFine	-0.612	-0.432	0.438	0.177	-0.468	0.098
Width	0.133	0.067	0.421	0.410	-0.181	-0.124
Depth	0.172	0.105	0.540	0.392	-0.187	-0.105
DepthSD	-0.215	-0.156	-0.295	-0.234	0.076	-0.020
Veloc	0.754	0.587	0.210	0.125	0.012	-0.067
VelocSD	0.502	0.332	0.225	0.254	0.021	-0.039
Cond	-0.331	-0.125	-0.557	-0.490	0.132	0.067

Evaluation of Fish Spawning Habitat Use in Relation to Substrate and Sediment Composition

Samples from spring 2014 are currently being processed. Results from spring 2013 are included here to illustrate potential differences among sites. Apparent fish eggs and larvae were collected on multiple dates at Kings Creek and Lawson's Fork Creek in spring 2013 (Table 7). Apparent fish eggs and larvae were collected from the Broad River immediately upstream of the confluence with the Tyger River and an apparent fish larva was collected from the Broad River downstream of the Tyger River. These specimens will be further examined and identified to the finest taxonomic level possible through consultation with experts. Once identifications are complete, differences in the presence and abundance (standardized by target taxa) of fish eggs and larvae among sites will be analyzed in relation to habitat/substrate, temperature and sediment levels. Shoals receiving and exhibiting greater quantities of fine sediment are expected to provide less suitable spawning habitat for certain fish species including rock/crevice spawners.

Influence of Sand Mining on Local Habitat, Sediment and Fish Assemblage Structure

Fourteen (14) fish species were collected altogether in fall 2013 and spring 2014 from the North Pacolet River adjacent to the active sand mine (Table 8). Species richness ranged from 8 (downstream, fall 2013 and spring 2014) to 10 (upstream, fall 2013). Sand extraction operations ceased indefinitely at the site in summer 2014; additional samples have been conducted and will continue at appropriate intervals in order to document potential changes in fish and habitat conditions associated with the termination of sand extraction. Analyses investigating differences between up- and downstream sites within and across sample periods and how these may be influenced by sand mining will continue.

Table 7. Preliminary results for fish egg and larva collections at study sites in the Broad River basin, spring 2013. Confirmation of fish origin and taxonomic identification are pending.

Date (2013)	Surber Sets	Kings Creek		Lawson's Fork Creek	
		Eggs	Larvae	Eggs	Larvae
23-Apr	10	0	0	1	1
2-May	10	3	0	0	0
10-May	10	0	0	No Sample	
14-May	10	2	0	1	0
21-May	10	8	0	0	1
30-May	10	0	2	No Sample	
Total		13	2	2	2

Date (2013)	Surber Sets	Broad River – Upstream of Tyger Confluence		Broad River – Downstream of Tyger Confluence	
		Eggs	Larvae	Eggs	Larvae
17-Apr	10	5	3	0	0
26-Apr	15	12	0	0	1
No additional samples conducted (high flows)					
Total		17	3	0	1

Table 8. Species abundance by sample for sites upstream versus downstream of an active sand mine on the North Pacolet River, Fall 2012 and Fall 2013.

	29 October 2013		23 May 2014	
	Downstream	Upstream	Downstream	Upstream
White Sucker	0	0	0	0
Notchlip Redhorse	2	0	0	0
Brassy Jumprock	3	0	0	0
Redbreast Sunfish	8	7	14	9
Warmouth	0	0	0	0
Bluegill	10	3	10	5
Largemouth Bass	0	0	0	0
Greenfin Shiner	1	31	7	43
Santee Chub	21	14	4	3
Bluehead Chub	13	12	7	21
Greenhead Shiner	0	1	0	7
Sandbar Shiner	0	0	0	18
Creek Chub	0	0	0	1
Flat Bullhead	0	2	1	0
Margined Madtom	2	6	1	1
Seagreen Darter	0	1	0	0
Eastern Mosquitofish	0	1	1	0
Species Richness	8	10	8	9
Total Fish	60	78	45	108

Discussion

In this analysis, fish assemblage structure varied in relation to a combination of natural site features (e.g. mean width, current velocity and elevation) and sediment-related conditions (e.g. d50, percent fine bed material and suspended sediment yield). The strength and direction of these relationships will be investigated further as more data become available. Because sedimentation of streams is largely related to land use and management practices, the existence of potential relationships between these measures and fish assemblage structure suggests that sediment control measures may have measurable conservation value for aquatic habitats and species in the Broad River basin.

Recommendations

Continue analyses with updated habitat, substrate and sediment data.

Examine relative influence of anthropogenic sediment impacts versus natural conditions on fish assemblage structure and aquatic habitat conditions in the basin.

Examine responses to changes in aquatic habitat and sedimentation among fish species, taxonomic and functional groups, including thresholds in habitat / sediment conditions at which populations or groups exhibit significant decline.

Incorporate findings into management guidelines to reduce negative impacts of sedimentation on aquatic habitats and species in the Broad River basin.

Literature Cited

Waters, T. F. 1995. Sediment in streams: sources, biological effects, and control. American Fisheries Society Monograph 7.

Job Title: Decision Support Tools for Stream Conservation

Period Covered July 1, 2013 – June 30, 2014

Summary

We completed deployment of the web-based South Carolina Stream Conservation Planning Tool, enabling a spatially-explicit understanding of how human activities affect the biological condition of wadeable streams. A web mapping application allows users to visualize predicted biological conditions based on their status and severity across all South Carolina wadeable stream catchments. Additionally, an interactive catchment management tool allows users to explore and forecast the impacts of customized land management scenarios on aquatic resource indicators at any user-specified stream location across South Carolina.

The application may be accessed and explored at this URL:

<http://54.204.4.5/scsa>

Introduction

This project is rooted in a watershed perspective that recognizes the pervasive nature of cumulative impacts to our waterways, and views a landscape approach as critical to successful aquatic conservation efforts. Fishery and aquatic scientists often assess habitats to understand the distribution, status, stressors, and relative abundance of aquatic resources. Due to the spatial nature of aquatic habitats and the increasing scope of management concerns, using traditional analytical methods for assessment is often difficult. However, advancements in the geographic information systems (GIS) field and related technologies have enabled scientists and managers to more effectively collate, archive, display, analyze, and model spatial and temporal data. For example, spatially explicit habitat assessment models allow for a more robust interpretation of many terrestrial

and aquatic datasets, including physical and biological monitoring data, habitat diversity, watershed characteristics, and socioeconomic parameters. The geospatial data produced as a result of this project proposal are intended to enable a unique, broad, and spatially explicit understanding of the links between natural habitat conditions, human influences on aquatic habitats, and aquatic ecosystem integrity. The ultimate goal is to improve understanding of how local and regional processes influence stream conditions in the state and to provide SCDNR with additional knowledge, data, and tools to help prioritize and drive conservation planning and action.

Materials and Methods

Data

The South Carolina Department of Natural Resources (SCDNR) in conjunction with Clemson University created this application using data from the South Carolina Stream Assessment, initiated in 2006 to determine the status of native fish assemblages and aquatic resources throughout the state. The assessment of nearly 500 wadeable streams was completed in 2011, with a collection of biological, chemical, physical, and landscape-level data necessary to support proactive decision making with respect to aquatic resources in the state. Sample locations were selected with a known probability using a stratified random sampling design from a list frame of all stream segments in the state, with ecobasin and stream size as strata. This site selection procedure insured independence among samples and allowed for statistically defensible estimates of statewide aquatic resource parameters.

From these data, we derived biological response variables designed to reflect biological/aquatic health and respond to anthropogenic stressors. We associated our biological

response variables with NHDPlus and National Fish Habitat Assessment spatial predictor data (USEPA and USGS 2005, Wang et al. 2011).

Modeling

We used Random Forests (Brieman 2001) with the R statistical software (R Core Team 2012) to develop predictive models from the sample data, from which we determined the most important spatial predictor variables that influenced each of the biological response variables. Using these modeled relationships from the sample data, we extrapolated to map current expected biological condition across the state based on spatial predictors.

Software

The application software design utilizes client- and server-side components. Dynamic ‘R’ prediction occurs on the server utilizing task parallelism. This allows simultaneous computation of predictions to occur. Client-side components use HTML5 and Javascript, which run entirely in the web browser. The mapper utilizes ArcServer 10.1 which allows for flexibility in geographic focus.

Results & Discussion

The Stream Conservation Planning Tool provides the following functionality:

- Map Viewer displays “static” predictions for South Carolina catchments based on extrapolations from random forest models. Each published predictive model includes a detailed PDF report describing response variable construction, random forest model results, model performance, and error metrics.
- Users can select catchments that drain an area of less than 150 sq km (wadeable streams).
- Anthropogenic variables that influence the model outcome are displayed.
- Users adjust these parameters using a sliding scale.

- Multiple catchments may be modified to scale up geographic area.
- The software recalculates attribute values for each selected catchment and conducts a downstream analysis (up until 150km² drainage limit is met).
- All downstream catchments impacted by modifications are returned to the user and displayed in the map.
- Users have access to prediction results for 24 hours and may export results in csv, or JSON formats.
- Administration privileges allow for application updates and revisions, including:
 - Upload prediction datasets.
 - Upload predictive models via a serialized R model using the native ‘RDS’ format.
 - Upload detailed model report as a PDF.
 - Set the attributes the user can modify (typically anthropogenic).

Recommendations

Continue outreach and education activities to build awareness of the application to potential user groups.

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Wang, L. , D. Infante , P. Esselman , A. Cooper , D. Wu , W. Taylor , D. Beard , G. Whelan and A. Ostroff. 2011. A hierarchical spatial framework and database for the National River Fish Habitat Condition Assessment. Fisheries 36(9): 436-449.

Job Title: Fish Community Response to Dam Removal in Twelvemile Creek, Pickens County, South Carolina

Period Covered July 1, 2013 – June 30, 2014

Summary

This progress report summarizes work done during the report period. Complete samples according to standardized methods described below were obtained in Fall 2013 and Spring 2014. The study is ongoing through 2016.

Introduction

Dams alter riverine environments by converting lotic habitats to lentic ones, thereby altering physical habitat, flow-regimes, temperature-regimes, sediment transport, dendritic connectivity, and nutrient cycling (Bednarek 2001). As a consequence, dams change the composition, structure, and function of native fish communities (Martinez et al. 1994, Taylor et al. 2001, Santucci et al. 2005). Few evaluations of the ecological effects of dam removal have been conducted in North America due to the lack of opportunity, particularly in the Southeast. A rare opportunity has presented itself with the removal of two mainstem dams on Twelvemile Creek, Pickens County, South Carolina (Figure 1).

Twelvemile Creek was extensively polluted with PCBs originating from a capacitor manufacturing plant from 1955-1975; the waste site and its receiving waters were listed with the EPA Superfund Program in 1990. Under CERCLA statute (Superfund law), a natural resources board of trustees is authorized to act as trustees of natural resources on behalf of the public, and within that role they may assess and recover damages for injuries and losses to natural resources caused by a hazardous waste site. As part of the settlement for damages caused by PCB

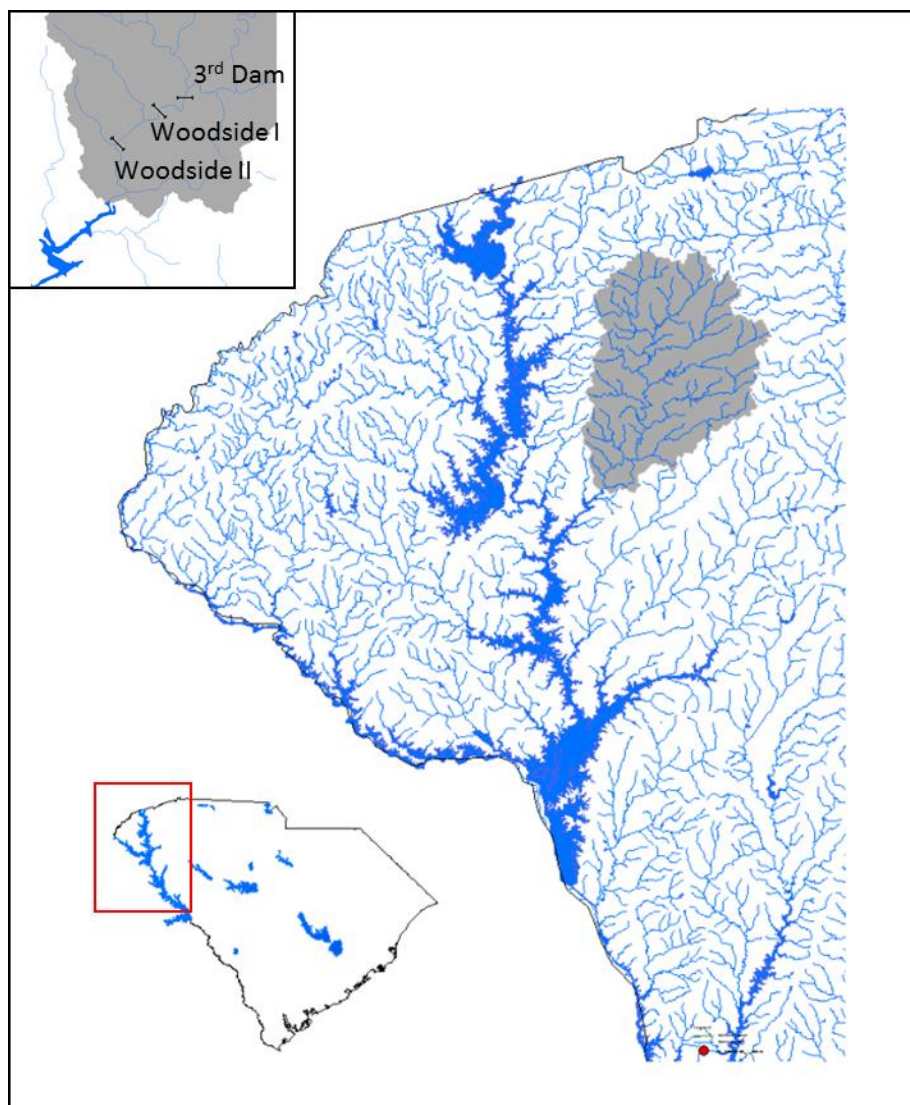


Figure 1. Twelvemile Creek drainage shaded in gray. Inset shows location of two former mainstem dams (Woodside I and Woodside II), and the remaining third dam (Easley-Central Dam).

contamination, a natural resources board of trustees facilitated the removal of two mainstem dams on Twelvemile Creek in order to 1) remove any remaining contaminated sediments that have accumulated behind the dams, and 2) to promote sediment transport to further ‘cap’ contaminated sediments downstream and in Lake Hartwell. Dam removal began in August 2009 with the initial dredging behind the upper dam (Woodside I); this dam was completely removed by April 2011. Dredging and removal preparations on the lower dam (Woodside II) began in April 2011, and removal was completed in September 2011.

The objective of this investigation was to document changes in the fish communities of Twelvemile Creek before and after the removal of the two dams (Woodside I and Woodside II). We have been monitoring fixed stations since 2006, and are scheduled to complete the study in 2016.

Materials and Methods

Six sampling stations were established for collecting biological and habitat data (Figure 1). The sampling stations are distributed as follows: 1) an alluvial stream section downstream of Woodside II Dam (Twelvemile Lower), 2) a bedrock-constrained free-flowing stream section downstream of Woodside II Dam (Woodside II Below), 3) an impounded area above Woodside II Dam (Woodside II Above), 4) a bedrock-constrained free-flowing stream section downstream of Woodside I Dam (Woodside I Below), 5) an impounded area above Woodside I Dam (Woodside I Above), and 6) an upstream reference station located upstream of both Woodside I and II, as well as upstream of a third dam (Robinson Bridge; Figure 1).

In addition, two sites on a nearby stream that has not been modified by dams, Three & Twenty Creek, were also established as additional reference. Those sites could not be sampled in Fall 2013 due to persistent high flows, but were sampled in Spring 2014

Fishes were collected at 20 wadeable stream segments of approximately 15m² within 300m segments at each site with a standardized effort using electrofishing gear and seines. All fishes encountered were collected, field identified to species level, recorded, and released. Habitat measurements of depth, velocity, and substrate were recorded at each of the 20 replicates; average widths were recorded at each site.

Results and Discussion

Total numbers of fish collected in October 2013 are shown in Table 1. May 2014 collections are shown in Table 2.

Recommendations

We will continue standardized sampling according to schedule at Twelvemile Creek and Three and Twenty Creek to provide a multi-year record of post dam-removal ecological conditions.

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Table 1. Summary of fish species and numbers collected in Twelvemile and Three and Twenty Creeks in October 2013.

Table 1. Summary of fish species and numbers collected in Twelvemile and Three and Twenty Creeks in October 2013.									
Species/Site	Robinson Bridge	Woodside I Above	Woodside I Below	Woodside II Above	Woodside II Below	Twelvemile Lower	3&20 LaFrance	3&20 Burns Bridge	Total
BBD	2	2	6	12	8	9	-	-	35
BHC	6	8	11	1	5	2	-	-	19
BLG	7	0	1	1	3	2	-	-	7
BLH	0	0	0	0	0	0	-	-	0
CCF	0	0	0	0	0	1	-	-	1
ESM	0	0	0	0	5	0	-	-	5
FBH	0	0	0	0	0	0	-	-	0
FCF	0	0	0	1	0	0	-	-	1
GSF	0	0	0	0	0	2	-	-	2
MGM	0	2	2	0	1	0	-	-	3
NHS	1	16	9	2	6	2	-	-	19
NLR	2	0	0	0	0	0	-	-	0
RBS	1	0	0	1	0	2	-	-	3
REB	1	0	0	0	1	2	-	-	3
RES	0	0	0	0	0	0	-	-	0
RFC	5	1	0	0	0	0	-	-	0
SBH	1	2	12	0	0	0	-	-	12
SPM	0	0	0	0	0	0	-	-	0
SPB	0	1	0	0	0	0	-	-	0
SPS	0	0	0	0	0	0	-	-	0
STJ	0	0	0	0	0	0	-	-	0
STS	0	0	3	34	79	53	-	-	169
SWD	0	0	0	0	0	1	-	-	1
TQD	0	5	8	10	3	1	-	-	22
WFS	2	1	3	55	35	45	-	-	138
YFS	4	9	3	2	19	5	-	-	29
YLP	0	0	0	0	0	0	-	-	0
Total Individuals	32	47	58	119	165	127	-	-	469
Taxa Richness	11	10	10	10	11	13	-	-	17

Table 2. Summary of fish species and numbers collected in Twelvemile and Three and Twenty Creeks in May 2014.

Species/Site	Robinson Bridge	Woodside I Above	Woodside I Below	Woodside II Above	Woodside II Below	Twelvemile Lower	3&20 LaFrance	3&20 Burns Bridge	Total
BBD	8	1	6	5	5	4	22	8	59
BHC	6	4	8	4	6	0	19	8	55
BLG	1	0	1	2	93	24	37	25	183
BLH	0	0	0	0	110	0	0	6	116
CCF	0	0	0	0	0	0	1	0	1
ESM	0	0	0	0	0	0	1	0	1
FBH	1	0	0	0	0	0	0	0	1
FCF	0	0	0	0	0	0	0	0	0
GSF	1	0	0	0	0	1	2	2	6
LMB	0	0	0	0	0	0	1	0	1
MGM	4	2	4	0	1	0	5	2	18
NHS	1	13	13	5	6	0	4	3	45
NLR	3	0	0	0	0	0	0	0	3
QLB	0	0	0	0	2	0	0	0	2
RBS	0	0	0	0	0	4	3	7	14
REB	0	0	0	0	1	0	0	3	4
RES	0	0	0	0	0	1	1	2	4
RFC	26	1	0	0	0	0	0	0	27
SBH	3	3	5	0	0	0	2	0	13
SPB	1	0	0	0	0	0	0	1	2
SPM	0	0	0	0	0	0	1	0	1
SPS	0	0	0	0	1	0	0	0	1
STJ	1	0	0	0	0	0	0	1	2
STS	0	0	2	29	115	90	16	40	292
SWD	0	0	0	0	0	0	0	0	0
TQD	0	4	12	4	12	0	0	0	32
WFS	0	1	2	1	32	10	4	12	62
WTP	0	0	0	0	15	0	0	0	15
YFS	6	1	2	0	1	0	3	0	13
YLP	0	0	0	0	254	2	0	1	257
Total Individuals	62	30	55	50	654	136	122	121	1230
Taxa Richness	13	9	10	7	15	8	16	15	28

Prepared By: Mark Scott, Troy Cribb,
Cathy Marion

Title: Wildlife Biologists

Job Title: Statewide compilation and assessment of crappie data

Period Covered July 1, 2013 – June 30, 2014

Summary

Portions of regional survey data from trapnetting and electrofishing for black crappie *Pomoxis nigromaculatus* from the past 10 years were received. Data was recieved from Regions 2 and 3 and compiled into a standard format for evaluation. In the coming year remaining data will be compiled. Variability in age and growth among populations and year classes, and efficiency of sampling strategies to collect data pertinent to crappie management will be assessed.

Introduction

In the last decade, a variety of methods have been used with varying success on reservoirs to assess crappie population dynamics. A compilation and analysis of crappie data from the last 10 years is underway. Efficiency of sampling strategies to collect data pertinent to management of crappie populations, and variability in age and growth among populations and year classes will be assessed. Of particular interest is the effect of recent implementation of an 8 inch size limit for crappie. At its conclusion study results will be communicated to regional staff. Findings will be discussed and future directions in crappie management considered.

Materials and Methods

Regional personnel were asked to provide data collected over the last 10 years in routine sampling of crappie. Data received was compiled into a standard format for pending analysis.

Results and Discussion

Trap net data was compiled and evaluated from Regions 2 (Lake Wylie) and 3 (Lake Murray). Lake Wylie data indicated a missing year class in 2006 sampling which led to a reevaluation of ageing data for all Lake Wylie collections from 2005-2007. This data was received late in the fiscal year, as was data for Lake Thurmond, and is not yet compiled.

Trap nets collect fish primarily in the age 0 – 3 year classes. A strategy to collect older fish from angler harvests was discussed but was not employed at this time. Crappie were collected by electrofishing in both Regions 2 and 3 during FY2014, and in the coming year this data will be compiled and electrofishing assessed as a means to collect older fish for population evaluations. Data from Lakes Thurmond and Greenwood will also be added to complete the compilation of historic data. This effort will continue in fiscal year 2015 and a strategy for addressing crappie management in South Carolina will be completed.

Recommendations

Continue study. Compile new and remaining data. Assess efficiency of sampling strategies to collect data pertinent to crappie management. Assess variability in age and growth among populations and year classes. Report on findings to regional staff.

Job Title: Identification and Distribution of crayfish in South Carolina

Period Covered July 1, 2013 to June 30, 2014.

Summary

A total of 2,883 unidentified crayfish were examined and identified to species, where possible. A total of 26 species of crayfish were identified in these samples. Distribution maps of crayfish in South Carolina was produced by combining this information with data held by Dr. Arnold Eversole, Clemson University. The full report of Dr. Eversole can be found at: <http://www.dnr.sc.gov/fish/fwfi/research.html> .

Introduction

Crayfish are an important aquatic taxon. Currently, 37 species are known to occur in South Carolina, of which 24 are currently considered 'priority conservation species. Additional taxonomic work was needed to better delineate species occurrences and abundance in South Carolina.

Materials and Methods

A total of 406 collections of crayfish from all counties of the State, obtained during the Statewide Stream Survey effort, had unidentified crayfish. These collections were sent to Dr. Arnold Eversole, Clemson University, for identification. Also, these records were added to the Eversole database to produce statewide distribution maps.

Results and Discussion

A total of 2,883 unidentified crayfish were obtained in the 406 collections sent to Dr. Eversole. Of these, approximately 10% of these were form I males, which are generally required for identification of crayfish species. All specimens were examined and 26 species were identified.

Distribution maps for the 37 species were generated, combining SCDNR data with Eversole data.

The full report of Dr. Eversole can be found at: <http://www.dnr.sc.gov/fish/fwfi/research.html> .

Recommendations

1. Work with Dr. Eversole to produce a useable 'Key to the Crayfish of South Carolina.'
2. Place taxa, life history information, and SC crayfish distribution maps on the SC DNR web site.
3. Where possible, obtain additional samples - and photos - of crayfish, especially from those counties that have received sparse coverage in the past.

Prepared By: James Bulak

Title: Research Coordinator, Freshwater
Fisheries

Job Title: Development of a Population Monitoring Plan for Broad River Smallmouth Bass

Period Covered July 1, 2013 – June 30, 2014

Summary

During 2014 we evaluated multiple pass depletion sampling as a method to estimate density and biomass of smallmouth bass *Micropterus dolomieu* in the Broad River. Twenty-five (25) hours of electrofishing effort were expended during four electrofishing passes of a 1,400 m sample reach. Fifty-six (56) smallmouth bass and 95 largemouth bass *Micropterus salmoides* were collected with a combined weight of 81 kg. We were not successful depleting smallmouth bass or largemouth bass within the sample reach with multi-pass sampling and consequently unable to produce reliable density and biomass estimates. Our initial effort was likely unsuccessful due to the large size (width and depth) of the selected sample reach.

Introduction

A thriving fishery for smallmouth bass exists in the Broad River; however, due to poor river access, poor capture efficiency, and difficult navigation a suitable method to assess the smallmouth bass abundance and population structure has not been developed. During 2014 we evaluated multiple pass depletion sampling as a potential standard sampling technique to evaluate smallmouth bass density, biomass, and population structure.

Materials and Methods

Multiple pass depletion sampling was conducted 29 October 2013 in a 1,400 m reach of the Broad River above Henderson Island. The river reach sampled was approximately 125 m wide, began just above Henderson Island (34.482339, -81.422734) and ended at the Tyger River

confluence (34.494867, -81.423318). Six electrofishing boats were spaced evenly across the river. Electrofishing was conducted continuously from the beginning to the end of the site and all *Micropterus* species encountered were collected. At the end of each pass fish were sorted by species, measured for Total Length (TL mm), weighed (g), and then placed in an oxygenated tank until the final pass was completed. After all sampling was completed the fish were released back into the sample reach.

Results and Discussion

Four electrofishing passes of the 1,400 m reach were completed with a total sampling effort of 25.3 hours. Electrofishing effort decreased each pass from 7.7 hours on the first pass to 5.8 hours on the last pass. A total of 95 largemouth and 56 smallmouth bass were collected (Table 1). We did not successfully deplete either species within the sample reach with multiple pass sampling and consequently were unable to produce reliable density and biomass estimates. Overall Mean TL of largemouth bass was 344 mm TL (Range; 190 – 570 mm TL) and overall mean TL of smallmouth bass was 296 mm TL (Range; 190 – 485 mm TL). Average weight was 616 g for largemouth bass and 405 g for smallmouth bass. The total biomass of collected fish was 58.6 kg for largemouth bass and 22.7 kg for smallmouth bass.

Table 1. Electrofishing pass number, number collected, mean total length (TL, mm) and weight (g), with range in parentheses, for *Micropterus spp* collected during 2013 from the Broad River, South Carolina with multi pass electrofishing.

Pass	N	Largemouth Bass		N	Smallmouth Bass	
		Mean TL	Mean Wt		Mean TL	Mean Wt
1	26	342 (239-430)	580 (162-1183)	21	286 (207-449)	342 (113-1122)
2	40	351 (221-492)	661(149-1836)	14	285 (201-485)	420 (105-1646)
3	9	335 (258-404)	514 (203-876)	10	286 (190-475)	374 (84-1609)
4	20	335 (190-570)	622 (77-2540)	11	340 (222-453)	536 (153-1296)
Total	95	344 (190-570)	616 (77-2540)	56	296 (190-485)	405 (84-1646)

Recommendations

Our multiple pass depletion sampling was not successful at estimating abundance or biomass of *Micropterus spp* in the Broad River. The sample site (1,400 x 125 m) was likely too large to successfully deplete the *Micropterus* population. The fourth pass was conducted during the evening with decreasing light levels. The number of both smallmouth bass and largemouth bass collected increased on the last pass, which may have been due to fish moving from deeper water, where they were not vulnerable to capture, to shallower water as light levels decreased. Although the multiple pass method was not successful on our first attempt it is recommended that the method is reevaluated on a smaller, and shallower reach of river.

Job Title: Great Pee Dee River Striped Bass

Period Covered July 1, 2013 - June 30, 2014

Summary

Genetic and movement information was obtained from adult striped bass *Morone saxatilis* collected in the North Carolina portion of the Great Pee Dee River. The information obtained from these fish indicated 1) there is some escapement of striped bass from NC reservoirs into the Great Pee Dee, 2) genetic population structure most closely resembled the Cape Fear/Roanoke rivers in NC, 3) there was migration of transmitted fish throughout the entire 324 km of the system, including the estuary, though the majority of time was spent in the most upstream reach, above Cheraw, SC.

Introduction

The Great Pee Dee River supports a population of striped bass. Little is currently known about the size, genetic make-up, or behavior of this species in this river system. Additional information was needed so that future management endeavors can develop appropriate procedures aimed at enhancing the population. The objectives of this work were to obtain a sample of striped bass for genetic characterization and, if possible, transmit several adult fish to assess seasonal movement patterns.

Materials and Methods

Efforts to collect adult striped bass were conducted in April and May of 2013 in the North Carolina portion of the Great Pee Dee River, from Blewett Falls dam downstream to the Jones Creek shoal. Efforts were coordinated with North Carolina Wildlife Commission and a multi-agency effort to collect robust redhorse. Boat electrofishing was the chosen collection method.

Fin clips were taken from all collected striped bass for genetic analysis using microsatellites. The fin clips were stored in vials containing sarcosyl urea and sent to the genetics lab at the Marine Division, SC Department of Natural Resources, for analysis. Twelve (12) microsatellite loci were assessed for each fish. All genetically assessed fish were then tested using PROBMAX3 and Cervus 3.0 parentage analysis software. All final determinations were based on Cervus statistics. STRUCTURE 2.3.4 was used to assess the genetic stock structure of Pee Dee River striped bass. Contrasts were made with reference collections obtained from the ACE basin (Ashepoo, Combahee, and Edisto rivers), Congaree River, Cooper River, Lake Marion, Lake Moultrie, Santee River, and Wateree River - all in South Carolina - and the Cape Fear and Roanoke rivers, North Carolina. Total length (TL), and in some instances, weights were also obtained from the collected striped bass.

On May 16, 2013 five adult striped bass were surgically implanted with Vemco acoustic transmitters. Approximately 58 remote receivers were already in place on the Great Pee Dee system for another project aimed at determining sturgeon movements. These receivers covered the entire Pee Dee system, from the Highway 17 bridge in Georgetown (designated as river km 0.0) to Cheraw, SC (river kilometer 301). Receivers were also located in Winyah Bay, downstream of the Highway 17 bridge and in the Waccamaw River; locations in these sites were given negative river kilometer designations to denote approximate distance from the Highway 17 bridge. Receivers were downloaded periodically and the location of each transmitted fish, by date and time of day, was recorded.

Results and Discussion

A total of 26 adult striped bass were collected for genetic analysis. Of these 26 samples were collected from the NC portion of the Pee Dee River, between the NC 74 bridge crossing and Jones

Creek shoal; fish were collected from April 14, 2013 to May 29, 2013. Average TL of collected striped bass was 642 mm with a minimum TL of 574 mm and a maximum length of 780 mm TL. One additional striped bass, 305 mm TL, was collected from the Great Pee Dee River on October 16, 2012 between the Cheraw and Society Hill, SC, sections of the river; it was included in the genetic analysis.

Parentage analysis indicated that 25 fish were designated as wild. One fish was defined as a cultured fish, originating from a North Carolina Wildlife Commission stocking in 2010. This fish was stocked into a North Carolina impoundments that is upstream of Blewett Falls dam.

Genetic population structure analysis indicated that these samples from the Great Pee Dee River most closely aligned with stocks found in the Cape Fear and Roanoke rivers, NC, though there was some signal from the Santee-Cooper system, SC, as well. The combination of populations in the samples indicated a mixed ancestry. This finding brings up the possibility that escapement from NC reservoir stockings dominate the current Pee Dee River stock; additional sampling of striped bass from downstream areas of the system is needed to evaluate this hypothesis.

Five adult striped bass were successfully implanted with acoustic transmitters on May 16, 2013. The identification number and total lengths of these fish were:

Transmitter 28409 - 703 mm, TL
Transmitter 28410 - 677 mm, TL
Transmitter 28411 - 657 mm, TL
Transmitter 28412 - 595 mm, TL
Transmitter 28413 - 780 mm, TL.

Four of five transmitted striped bass provided movement and residency information during the study year. Two days after capture, fish 28409 moved away from the area of collection, moving

downstream approximately 250 km in three days. After this initial migration, it spent the majority of its time in the lower 50 kilometers of the basin, including Waccamaw River and Winyah Bay (Figure 1). The last detection of this fish was made on July 25, 2013 at the Bull Creek entrance to Waccamaw River; it was assumed this fish either died or was harvested.

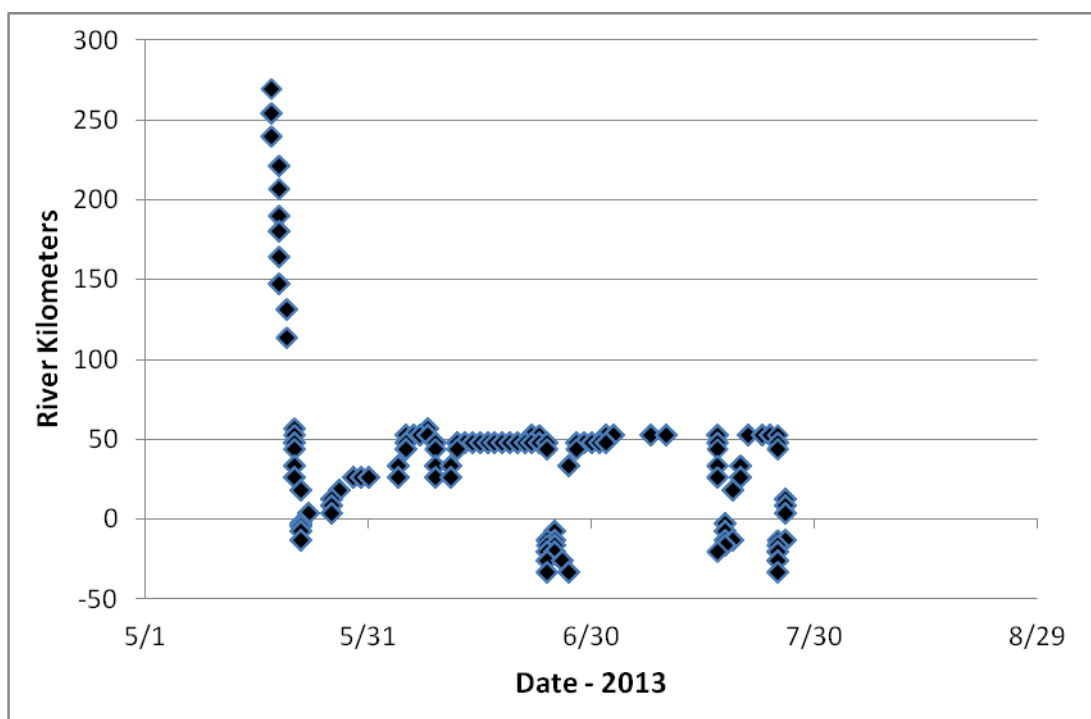


Figure 1. Movement of striped bass 28409 in the Great Pee Dee River basin, South Carolina. The fish (703 mm total length) was tagged at approximately river kilometer 309, 15 km below Blewett Falls dam. River kilometer 0.0 was the Highway 17 bridge. Negative river kilometers designate movement into either Waccamaw River or Winyah Bay.

Striped bass 28410, 28411, and 28412 all stayed near the NC tagging site until October 2013. Fish 28411 exhibited the most movement, traveling downstream approximately 250 km in four days in mid-October, spending 6 weeks in the most downstream 50 km section, and then returning in early December to the tagging site; substantial downstream migrations were also noted in late winter and spring of 2014 (Figure 2). Fish 28410 migrated downstream to river km 78 during a 9 day period of late October/early November and apparently stayed in that area until early April of 2014 (Figure 3).

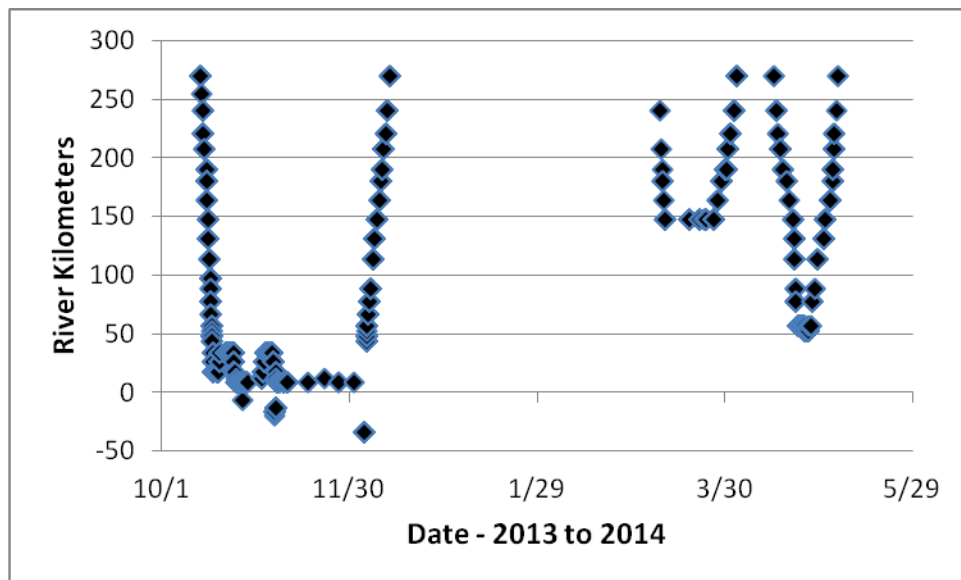


Figure 2. Movement of striped bass 28411 in the Great Pee Dee River basin, South Carolina. The fish (657 mm total length) was tagged at approximately river kilometer 309, 15 km below Blewett Falls dam. River kilometer 0.0 was the Highway 17 bridge. Negative river kilometers designate movement into either Waccamaw River or Winyah Bay.

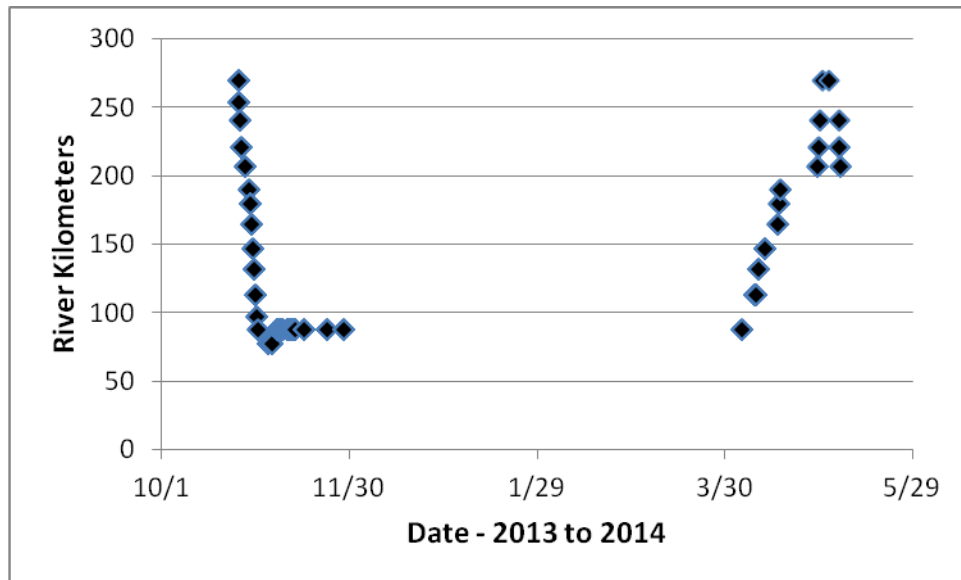


Figure 3. Movement of striped bass 28410 in the Great Pee Dee River basin, South Carolina. The fish (677 mm total length) was tagged at approximately river kilometer 309, 15 km below Blewett Falls dam. River kilometer 0.0 was the Highway 17 bridge.

In mid-October, fish 28412 moved downstream in one day to river kilometer 200, stayed there for approximately one month, returned in early December to the area of tagging, and apparently stayed in the most upstream area through May of 2014 (Figure 4).

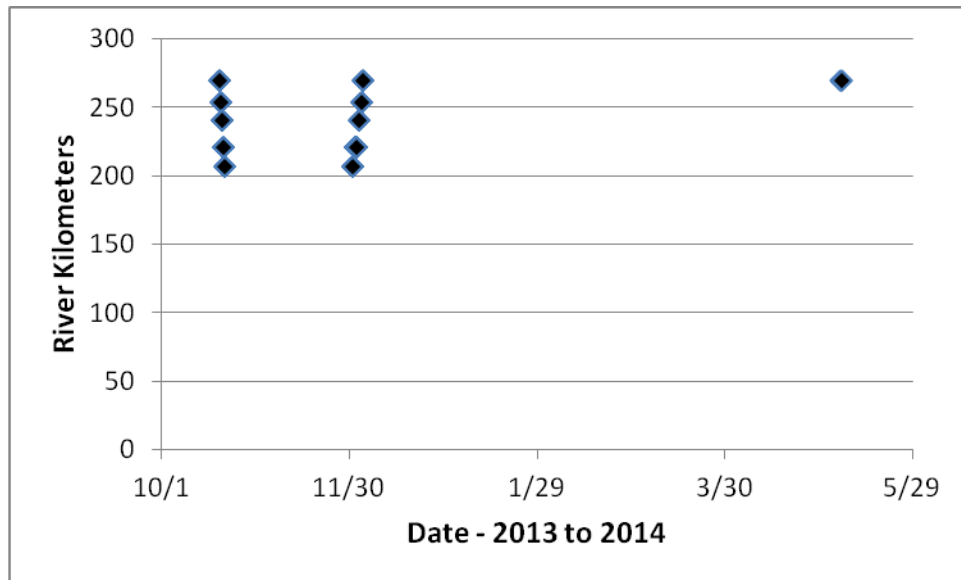


Figure 4. Movement of striped bass 28410 in the Great Pee Dee River basin, South Carolina. The fish (677 mm total length) was tagged at approximately river kilometer 309, 15 km below Blewett Falls dam. River kilometer 0.0 was the Highway 17 bridge.

Recommendations

1. Obtain additional samples for genetic evaluation from downstream areas of the Pee Dee River to assess whether there is longitudinal segregation of sub-stocks.
2. Do not stock Great Pee Dee until additional genetic population structure information is obtained. If stocking must occur prior to obtaining this information, use of NC strain fish in the upper reaches (Cheraw) appears to be the preferred action.
3. Transmit additional striped bass collected from downstream areas of the Pee Dee River to discern if movements of those fish would be similar to the currently transmitted fish.

4. Movement data suggests that striped bass spawn between Blewett Falls dam and Cheraw. When resources allow, more fully access the magnitude of spawning.

